

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 12:54:35 ; Search time 19513.3 Seconds  
(without alignments)  
17420.151 Million cell updates/sec

Title: US-10-781-979-1  
Perfect score: 5980  
Sequence: 1 tacatgcaatacataaagag.....ttctaaaaagcctctgtat 5980

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_in.\*
- 3: gb\_env.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pr.\*
- 9: gb\_ro.\*
- 10: gb\_sts.\*
- 11: gb\_sy.\*
- 12: gb\_un.\*
- 13: gb\_vi.\*
- 14: gb\_htg.\*
- 15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 5980  | 100.0       | 5980   | 6     | CQ868311 Sequence |
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| 3          | 2233  | 37.2        | 4100   | 1     | AB112346 Bacillus |
| 4          | 2082  | 34.8        | 2082   | 6     | CQ868312 Sequence |
| 5          | 2073  | 34.7        | 2073   | 6     | CQ868314 Sequence |
| 6          | 1686  | 28.2        | 1686   | 6     | CQ868316 Sequence |
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| 8          | 1038  | 17.4        | 3752   | 1     | AB125059 Bacillus |
| 9          | 967   | 16.2        | 4331   | 1     | BTJSG65           |
| 10         | 966   | 16.2        | 3931   | 1     | AB161456          |
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| 12         | 891   | 14.9        | 3642   | 1     | AB193814          |
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| 14         | 855   | 14.3        | 2145   | 6     | CQ868324          |
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| 16         | 790   | 13.2        | 4186   | 6     | E01905            |
| 17         | 789   | 13.2        | 3684   | 1     | BTITOX            |
| 18         | 789   | 13.2        | 3684   | 1     | BTTOXD2           |

|    |     |      |        |   |             |                    |
|----|-----|------|--------|---|-------------|--------------------|
| 19 | 789 | 13.2 | 3684   | 6 | I08884      | 108884 Sequence 2  |
| 20 | 787 | 13.2 | 3535   | 6 | I06096      | 106096 Sequence 2  |
| 21 | 776 | 13.0 | 4253   | 1 | BACLSRH4    | D00248 Bacillus th |
| 22 | 776 | 13.0 | 127923 | 1 | BTPTOXIS    | AL731825 Bacillus  |
| 23 | 774 | 13.0 | 4934   | 6 | E01676      | E01676 DNA sequenc |
| 24 | 769 | 12.9 | 4451   | 6 | I08083      | I08083 Sequence 1  |
| 25 | 769 | 12.9 | 4056   | 1 | I09103      | I09103 Sequence 1  |
| 26 | 768 | 12.9 | 4056   | 1 | BACCRD2     | M20242 B.thuringie |
| 27 | 765 | 12.8 | 3543   | 1 | BTTOXD1     | Y00423 Bacillus th |
| 28 | 747 | 12.5 | 2019   | 6 | CQ868325    | CQ868325 Sequence  |
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| 33 | 400 | 6.7  | 3756   | 1 | E00614      | E00614 DNA encodin |
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| 36 | 380 | 6.5  | 4359   | 6 | AX670917    | AX670917 Sequence  |
| 37 | 383 | 6.4  | 1738   | 6 | I03580      | I03580 Sequence 3  |
| 38 | 380 | 6.4  | 3504   | 6 | BD133574    | BD133574 Protein h |
| 39 | 380 | 6.4  | 3690   | 6 | BD133575    | BD133575 Protein h |
| 40 | 362 | 6.1  | 3483   | 1 | BTU04366    | U04366 Bacillus th |
| 41 | 360 | 6.0  | 3483   | 1 | AY518201    | AY518201 Bacillus  |
| 42 | 358 | 6.0  | 3797   | 6 | AR005118    | AR005118 Sequence  |
| 43 | 358 | 6.0  | 3797   | 6 | AR050172    | AR050172 Sequence  |
| 44 | 358 | 6.0  | 3797   | 6 | E06830      | E06830 DNA sequenc |
| 45 | 356 | 6.0  | 3435   | 1 | AB089299    | AB089299 Bacillus  |

ALIGNMENTS

|            |  |                                       |         |     |        |                 |
|------------|--|---------------------------------------|---------|-----|--------|-----------------|
| RESULT 1   | CQ868311   | Sequence 12 from Patent WO2004074462. | 5980 bp | DNA | linear | PAT 14-SEP-2004 |
| LOCUS      | CQ868311   |                                       |         |     |        |                 |
| DEFINITION | CQ868311   |                                       |         |     |        |                 |
| ACCESSION  | CQ868311   |                                       |         |     |        |                 |
| VERSION    | CQ868311.1   | GI:51998357                           |         |     |        |                 |
| KEYWORDS   |  |                                       |         |     |        |                 |
| SOURCE     | Bacillus thuringiensis                                     |                                       |         |     |        |                 |
| ORGANISM   | Bacillus thuringiensis                                     |                                       |         |     |        |                 |
| REFERENCE  | 1  |                                       |         |     |        |                 |
| AUTHORS    | Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B. |                                       |         |     |        |                 |
| TITLE      | Delta-endotoxin genes and methods for their use            |                                       |         |     |        |                 |
| JOURNAL    | Patent: WO 2004074462-A 12 02-SEP-2004;                    |                                       |         |     |        |                 |
| FEATURES   | Athenix Corporation (US)                                   |                                       |         |     |        |                 |
| source     | Location/Qualifiers  |                                       |         |     |        |                 |
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| ORIGIN | Query Match           | 100.0%  | Score 5980;   | DB 6;     | Length 5980; |
|        | Best Local Similarity | 100.0%  | Pred. No. 0;  |           |              |
|        | Matches 5980;         | Conservative 0;   | Mismatches 0; | Indels 0; | Gaps 0;      |
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| Db     | 1                     | TACATGCAATACATAAAGAGAGGTTTAAATAATCAATACCTCACCACCAATAATGGGTT | 60            |           |              |
| QY     | 61                    | TATTTGTAGAAACATTTGTACAGGAATACATTTGGGTACTACGATATATAGAAAACAC  | 120           |           |              |
| Db     | 61                    | TATTTGTAGAAACATTTGTACAGGAATACATTTGGGTACTACGATATATAGAAAACAC  | 120           |           |              |
| QY     | 121                   | CTAACATATATTTATTAGTGCTCTTAAATAAGAGTATATAGAGGAGTAAACATGA     | 180           |           |              |
| Db     | 121                   | CTAACATATATTTATTAGTGCTCTTAAATAAGAGTATATAGAGGAGTAAACATGA     | 180           |           |              |
| QY     | 181                   | GTCCATATCAAAATAAAAAATGAATATGGAATCTTCATCGAATAACACAAATA       | 240           |           |              |



|    |      |  |      |
|----|------|--|------|
| Qy | 2401 | TATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAAACTGGC      | 2460 |
| Db | 2401 | TATGTCAGATGAACAAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAAACTGGC      | 2460 |
| Qy | 2461 | AAAACAACTTAGTCAGTCTCGTAATCTACCTCCAAAATGGAGACATTTTCTGGGAATGATTG   | 2520 |
| Db | 2461 | AAAACAACTTAGTCAGTCTCGTAATCTACCTCCAAAATGGAGACATTTTCTGGGAATGATTG   | 2520 |
| Qy | 2521 | GACATTCGGTAATGATATTATCATAGGATCCAAATAATCCTATTTTAAAGGAAAAATTTCT    | 2580 |
| Db | 2521 | GACATTCGGTAATGATATTATCATAGGATCCAAATAATCCTATTTTAAAGGAAAAATTTCT    | 2580 |
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[illegible]

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DEFINITION  
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Bacillus thuringiensis serovar aizawai cry40A and 40orf2 genes for putative mosquitocidal toxin and Cry40ORF2 protein, partial and complete cds.  
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VERSION  
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KEYWORDS  
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SOURCE  
Bacillus thuringiensis serovar aizawai  
ORGANISM  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE  
1 Ito, T., Sahara, K., Asano, S. and Bando, H.  
Cloning and Expression of Novel Crystall Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins Unpublished  
2 (bases 1 to 3746)  
Ito, T., Sahara, K., Asano, S. and Bando, H.  
Direct Submission  
Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Kita-9Jyou Nishi-9chome, Kita-ku, Sapporo-shi, Hokkaido 060-8589, Japan  
(E-mail: ito-t@abs.agr.hokudai.ac.jp, Tel:81-011-716-2487)

FEATURES  
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ORIGIN

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QY 775 TATTAAAGGATGAGTTCATATATAAGACCAATGTTTCCCATTTTGGTGGCAGAGAAATG 834  
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DB 840 GTAGAGAAATGAGCTTTGACCGGTATTCGATATATATCCTATATTTTCAAACTTATGATTTTC 899  
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DB 1320 CATTTATATACCTGTTATGATCAGGTAATGTTGGGCTAAGCAGCATGACAAATTTACATCTA 1379  
QY 1555 CGTCCCACTTGTATTTGCACTCTAA---TGGTGTTAGAGGACCCCTCTCATAGATTATCAA 1611  
DB 1380 AGTTACCGGATTTAAGAAATCCAGAACTTAGTTATAGAGATTACTCTCATAGATTATCAA 1439  
QY 1612 ATGCGGCATGTTGTTATATGGAACCTCCAGAGTTAACGTTATATGTTTGGACACATACAA 1671  
DB 1440 ATGCGGCATGTTGTTGAGCTGGCAACAGCAGAAATTAACGTTATATGTTTGGACACATACAA 1499  
QY 1672 GTTTTAAACGCTGAAATATAATTTGAAGCCAATCAAAATTAACAAATACCGGGGCTGAAGA 1731  
DB 1500 GTATGTCAAAATATTAATCTTAATTTTCCAGACAAATTAACAAATACCGGGGCTGAAG 1559  
QY 1732 GTTATTTACCTTCAAAATTTATCTTGGTAAATGCCTATACCTTATGTAATAAAGGCATCTATA 1791  
DB 1560 CTTTGTGATATACGGAT-----ACAGGCGCCAGGTC 1589  
QY 1792 CAGTGGGGATTTAATCCGTTTAAAGAAACAAATACAGAGTATAACCGAGTTTATGTCAG 1851  
DB 1590 AAGTCATAGCTGACCTGCTGATACAGGAGGAAATGTAGTAAGCTTTACCATATATTATTCAC 1649  
QY 1852 GTGGCGGAATAGATTGATTATTAATAACAAACTGCAGGACAAAGTTCACCGTATTTTCGTT 1911  
DB 1650 GTTTTAAATAACGTTTAAATTCCTGATCCCAAT-----AAATAATCTTGTGTAGAG 1703  
QY 1912 TTCGTTATCTGCAGATAAAGCTGCTTCTTTAGTGTATATCTTTTATCCAGGAGGTGGG 1971  
DB 1704 TTCGCTATACAAGTACAGCAATGGTAGGTACTAGTAAAGATGGTCCGCCGAGTTCTA 1763

|    |      |   |      |
|----|------|---|------|
| Qy | 1792 | GTTCAAATCGTTTTGTATCGCTTGAAAAATCTTTACTCTGAAAAATTATGACGATTTAAAAAT     | 2031 |
| Db | 1764 | TTATAAATAGTATATTTTTTTCTTCCATCTACGGGTCTGTGTGATTCATTTTGGCTATGTGG      | 1823 |
| Qy | 2032 | ATAGTGATTTTAAATTCGCTGAAATTTATCACACCTCCATTACCTAGTTTCAAAATTCAGA       | 2091 |
| Db | 1824 | ACA-----CCTTAGTTTACTACATTTTAATTCAGC                                 | 1850 |
| Qy | 2092 | TGGATGTGGAGATCAAGCGAATAGTTTTCAATCAGATGTAAACGTGGTTCTCGACAAAA         | 2151 |
| Db | 1951 | CAGGTGTGAATTAATTTATACAAATCTTGNATACCCCTATTACG-----TTGACAAAG          | 1904 |
| Qy | 2152 | TTGAATTCCTCCCAAGTAATACAACTTTTAGAATATGAGGGAGAACGGGACCTAGAAA          | 2211 |
| Db | 1905 | TTGAATTTATCCCACTCAATTTCTACGGCCTTAGAAATATGAAGGAAAAACAAGTCTAGAAA      | 1964 |
| Qy | 2212 | AAAACAAAGAACCGGTGGAACGATCTGTTTACCRAATTAACAAATTAATTTACTTAGNATA       | 2271 |
| Db | 1965 | AGGCACAGATGTAGTGAATGATTTATTTGTAAAGTAAAAATAAAGT-ATGTACGAAGTA         | 2023 |
| Qy | 2272 | GGTGATTTGCTGTTTAAACAAATAAGCGAAAAAGGTTGTAGTCCCTATGTTTACAAGTAG        | 2331 |
| Db | 2024 | GGGGTATCGTTGATTAACAAATACGCGAAAAAGGTTGTAGTCCCTATGTTTACAATGG          | 2083 |
| Qy | 2332 | TACGAAAAATACGTTTAAAAATAGAAAAACACAGATTTGAAATAGATCAAGCGGCCATTTTC      | 2391 |
| Db | 2084 | TACGAAAAATACGCTGAAAAATAGAAAAACACAGATTTAGAAATAGATCAAGCGGCCATTTTC     | 2143 |
| Qy | 2392 | TATAGAATGTATGTCAGATGAACAAATCCTCAGGAAAAAATTAATGTTATGGGATGAAAT        | 2451 |
| Db | 2144 | GATAGAATGTATGTCAGATGAACATCTCCCTAAAGAAAAAATGATGTTATGGGATGAAAT        | 2203 |
| Qy | 2452 | AAAACTGGCAAAACAACTTAGTCAAGTCTCGTAATCTACTCCAAAA-----TGGAGA           | 2502 |
| Db | 2204 | AAAAAGGCAAAACTACTTAGTCAGTCTCGTAAATTTTACTCCAAAAATGGGGACTTTGGAGA      | 2263 |
| Qy | 2503 | CTTTTCTGGGAATGATTTGGACATTTGGTAAATGATATTATONTAGGATCCAAATATCCTAT      | 2562 |
| Db | 2264 | CTTTTATGGAAATGATTTGGAAATTTCCGGTAAATTAATTTATCATAGGATCCAAATATTTCTAT   | 2323 |
| Qy | 2563 | TTTTTAAAGGAAAAATTTCTACAGATGCGTGGAGCACGAGACATATATCGAACTCTATTTCC      | 2622 |
| Db | 2324 | TTTTTAAAGGAAAAATTTCTTCAGATGAGTGGAGCCGAGACATATATGGAACTATATTTCC       | 2383 |
| Qy | 2623 | AACCTATATCTGTCAAAAAATAGATGAGTCTTAAATTAACCAATATACACGTTATCGAGT        | 2682 |
| Db | 2384 | AACCTATATCTATCAAAAAATAGATGAATCTTAAATTAACCAATATACACGCTATCGAGT        | 2443 |
| Qy | 2683 | AAGAGGGTTTGTGGGAAGTAGTAAAGATTTGMAATTAATGGTAAACAGTTTACGGGAAGA        | 2742 |
| Db | 2444 | AAGAGGGTTTGTGGGAAGTAGTAAAGATCTAAGATTTGATGGTAAACAGTTTACGGGAAGA       | 2503 |
| Qy | 2743 | AATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTTATATGTCAGCTTAATCTCTCATG      | 2802 |
| Db | 2504 | AATTGATGCCATGATGAATGTTCCAAATGATTTGGCCTTATATGTCAGCTTAATCTCTCATG      | 2563 |
| Qy | 2803 | TGGAGATTTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAAGGGTATCTTACACCAAC      | 2862 |
| Db | 2564 | TGGAGATTTCTCGCTGTGAATCATCGTCTCCAGTATGTGAGCCAAAGGGTATCTTACACCAAC     | 2623 |
| Qy | 2863 | AGATGGATATGCTCCCGNATGTTATGATGATGCCCAAAATATAGATAGAAGCATGTGAA         | 2922 |
| Db | 2624 | AGATGGATATGCTCTGATAGGTATGATGCGCCGTCAGGTTTTCAGTAAAAAACAATGTTAT       | 2683 |
| Qy | 2923 | GTGTACAGATCGTCAATTTGATTTTTCATATTTGACACCGGAGAAAGTAGATACAAATAC        | 2982 |
| Db | 2684 | GTGTACAGATCGTCAATTTGATTTTTCATATTTGACACCGGAGAAATAGATACAAATAC         | 2743 |
| Qy | 2983 | AAATGTAGGATTTGATGTCATTATAAAAAATTTCTTAATCTCAGATCGGATACGCTACAGTAGG    | 3042 |
| Db | 2744 | AAAAGTAGGATTTGATGTCATTATTTTAAAAATTTCTTAATCTCAGATCGGATGATGCTACATPAGG | 2803 |

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|----|------|--|------|
| QY | 3043 | GAATCTAGAGTCAATTGAGAGGACCACTAAACAGGTGAAGCAATTGGCACAATGTGAACA     | 3102 |
| DB | 2804 | GAATCTAGAGTCAATTGAGAGGCGGCACCTAAACAGAGGAAGCAATTAAACGATGTGAACA    | 2863 |
| QY | 3103 | AAAGGAAAGAAATGGGAAAACAACATCGGAGAAAACGTTGGGAAAACAACAAGGCTA        | 3162 |
| DB | 2864 | AAAGGAAAGAAATGGGAAAACAACATCGGAGAAAACGTTGGGAAAACAACAAGGCTA        | 2923 |
| QY | 3163 | TGATCCAGCAAAACAGGCTGTAGATGCATTATTTTACAATGAACAAGAGTTACATATCA      | 3222 |
| DB | 2924 | CGATCCAGCAAAACAGGCTGTAGATACATTTATTACAATGAACAAGAGTTACATATCA       | 2983 |
| QY | 3223 | TATTACTTTAGATCATATTCOAACCGTGTAGCTGGTACAGTCGATTCCTTATGTATA        | 3282 |
| DB | 2984 | TATTACTTTAGATTTATATTC-AAAACGCTGTAGCTAGCTGGTACAGTCGATTCCTTATATA   | 3042 |
| QY | 3283 | CCATAATTGGTTACC-GAATGCTCCAGGTATGAACATATGATATCAAGAGTTAAACG        | 3341 |
| DB | 3043 | CCATGACTGGTTACCGGATGCCCGAGTATGAACATATGATGATATCAAGGGTTAAACG       | 3102 |
| QY | 3342 | CACGTATCATGCAAGGTTATAAATTTATATGATGCACGAAATGTCATAACAATGGTGACT     | 3401 |
| DB | 3103 | CACGTATCATGCAAGGCTACAAATTTATATGATGCACGAAATGTCATCACAATGGTGACT     | 3162 |
| QY | 3402 | TTACACAAGGATTAACAGGATGGCAACCAACAGGAAATGCCGGGTACACAATAATGGATG     | 3461 |
| DB | 3163 | TTACAACAAGGATTAACAGGATGGCAACGACGACGCGGAAAGGACGCGGTACACAAGATCGATG | 3222 |
| QY | 3462 | GAGCTTCAGATTAATAGTTCTCATCAAAATGGAGCGCGGGGTATCTCAAAACTTCGATGCTC   | 3521 |
| DB | 3223 | GCGCTTCTGTATTAGTTCTCATCAAACTGGAGTGGCGGGGTATCTCAAAATCTGATGCTC     | 3282 |
| QY | 3522 | AAGATCATCATGGATATGTGTTCAGTGTGATTCGCAAAAAGAGGACCTCGAAAAGGGT       | 3581 |
| DB | 3283 | AAGATCATCATGGATATATGTTCAGTGTGATTCGTAATAAAGAGGACCTCGAAAAGGGT      | 3342 |
| QY | 3582 | ATGTAACGATGATGGATGTAAATGGAAAGCAGGAAACACTTAAGTTCACCTTCCTGCGAAG    | 3641 |
| DB | 3343 | ATGTAACGATGATGGATGTAAATGGCAATCAGGAAACACTGAAGTTCACTTCCTGTGAAG     | 3402 |
| QY | 3642 | AAGGATATATGACAAAACAGTAGAGGTATTCGCAAGAAAGTATCGGTACGGATTCGAAA      | 3701 |
| DB | 3403 | AAGGATATATGACAAAACAGTAGAGGTATTCGCAAGAAAGTATCGGTACGGATTCGAAA      | 3462 |
| QY | 3702 | TAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTTTGTATGCAAGGAT     | 3761 |
| DB | 3463 | TAGGAGAAACCGAAGGTACGTTTATATGATAGCATCGAGTTGCTTTGTATGCAAGGAT       | 3522 |
| QY | 3762 | ATGATAACAATAATAA-CTGTCACACGGGTAAATATGATGAGCAAGATTATAATGGAAATT    | 3821 |
| DB | 3523 | ATGCTAGCAATAATAA-CCGACACGGGTAAATATGATGAGCAAGATTATAATGGAAATT      | 3582 |
| QY | 3822 | ATAATCAAAATACCTAGCGATGTGTTATCAAGGGTATACAAACACTATAACCAAGACT       | 3881 |
| DB | 3583 | ATAATCAAAATACCGAGCGATGTGTTATCAAGGGTATACAAACACTATAACCAAGACT       | 3642 |
| QY | 3882 | CTAGTAATATGTATAAATCAAAATTTACTTAACAAATGATGACCTGCTTCGGTTGCACAT     | 3941 |
| DB | 3643 | CTAGTAATATGTATAAATCAAAATTTACTTCAATGATGACCTGCTTCGGTTGCACAT        | 3702 |
| QY | 3942 | GTAACCAAGGCGATAACTCTGGCTGTATCATGTAAATCAAGGATA                    | 3984 |
| DB | 3703 | GTAACCAAGGCGATAACTCTGGCTGTATCATGTAGTCAAGGATA                     | 3745 |

|            |           |
|------------|-----------|
| RESULT 3   | ACCESSION |
| AB112346   | VERSION   |
| LOCUS      |           |
| DEFINITION |           |









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CQ868314  
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DEFINITION Sequence 15 from Patent WO2004074462.  
ACCESSION CQ868314  
VERSION CQ868314.1 GI:51998360  
KEYWORDS  
SOURCE Bacillus thuringiensis  
ORGANISM Bacillus thuringiensis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus source.  
1  
REFERENCE  
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.  
TITLE Delta-endotoxin genes and methods for their use  
JOURNAL Patent: WO 2004074462-A 15 02-SEP-2004;  
Athenix Corporation (US)  
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AVNDLFTN"

Query Match 34.7%; Score 2073; DB 6; Length 2073;  
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## RESULT 6

CQ868316 LOCUS 1686 bp DNA linear PAT 13-SEP-2004  
DEFINITION Sequence 17 from Patent WO2004074462.  
ACCESSION CQ868316  
VERSION CQ868316.1 GI:51998362

## KEYWORDS

SOURCE

ORGANISM

Bacillus thuringiensis  
Bacillus thuringiensis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

## REFERENCE

1.  
Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.  
Delta-endotoxin genes and methods for their use  
Patent: WO 2004074462-A 17 02-SEP-2004;  
Athenix Corporation (US)

## FEATURES

source

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TITLE Cloning and Expression of Novel Crystal Protein Genes cry39A and 39orf2 from *Bacillus thuringiensis* subsp. *aizawai* Bunl-14 Encoding Mosquitocidal Proteins

JOURNAL Insect Biotechnol. Sericulture 71, 123-128 (2002)

REFERENCE 2 (bases 1 to 3727)

AUTHORS Ito, T., Sahara, K., Asano, S. and Bando, H.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Applied Bioscience, Kita 9-jyo, Nishi 9-chome, Kita-ku, Sapporo, Hokkaido 060-8589, Japan (E-mail: ito-t@ab.sagr.hokudai.ac.jp, Tel: 81-011-706-2487, Fax: 81-011-706-2487)

COMMENT On Mar 12, 2002 this sequence version replaced gi:16945768.

FEATURES

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## ORIGIN

Query Match 25.58; Score 1526.4; DB 1; Length 3727;  
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RESULT 8

AB125059 3752 bp DNA linear BCT 28-OCT-2003  
LOCUS  
DEFINITION  
Bacillus thuringiensis serovar entomocidus cry30Aa like gene for putative moquitocidal toxin and hypothetical protein gene, complete cds.

ACCESSION  
VERSION  
AB125059  
AB125059.1 GI:37999233

KEYWORDS

SOURCE  
ORGANISM  
Bacillus thuringiensis serovar entomocidus  
Bacillus thuringiensis serovar entomocidus  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE  
AUTHORS  
TITLE  
Ikeya, T., Yamaya, K., Ito, T., Sahara, K., Bando, H. and Asano, S.  
Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. entomocidus INA288

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (24-OCT-2003) Tomonori Ikeya, Graduate School of Agriculture, Hokkaido University, Department of Applied Bioscience, Kita-9-jo, Nishi-9-chome, Kita-ku, Sapporo, Hokkaido 0608589, Japan (E-mail: ikeyan@ab.agr.hokudai.ac.jp, Tel: 81-011-706-2487 (ex. 2487), Fax: 81-011-706-2487)

FEATURES  
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ORIGIN

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RESULT 11

AB185105

LOCUS

DEFINITION

AB185105

Accession

Version

Keywords

Source

Organism

3668 bp

DNA

linear

BCT 23-JUL-2004

Bacillus thuringiensis cry24-like, orf281 genes for

delta-endotoxin, hypothetical protein, complete cds.

AB185105.1

GI:50539654

Bacillus thuringiensis

Bacillus thuringiensis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

1

Ohgushi,A., Saitoh,H., Wasano,N. and Ohba,M.

Cloning and characterization of novel cry genes from a

mosquitocidal Bacillus thuringiensis serovar sotto strain

Unpublished

2 (bases 1 to 3668)

Ohgushi,A., Saitoh,H., Wasano,N. and Ohba,M.

Direct Submission

Submitted (16-JUL-2004) Akira Ohgushi, Kyushu University, Graduate

School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka,

Fukuoka 812-8581, Japan (E-mail:ohgushi@brs.kyushu-u.ac.jp,

Tel:81-92-642-3028, Fax:81-92-642-3028)

Location/Qualifiers

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Query Match 15.6%; Score 935.4; DB 1; Length 3668;

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Source

AB193814 3642 bp DNA linear BCT 28-OCT-2004  
Bacillus thuringiensis gene for Cry30-like, hypothetical protein,  
complete cds.  
AB193814  
AB193814.1 GI:54695304  
Bacillus thuringiensis  
Bacillus thuringiensis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1. Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.  
Identification and characterization of novel cry genes from an  
mosquito-specific *Bacillus thuringiensis* serovar sotto strain  
unpublished  
2 (bases 1 to 3642)  
Ohgushi, A., Wasano, N., Saitoh, H. and Ohba, M.  
Direct Submission  
Submitted (26-OCT-2004) Akira Ohgushi, Kyushu University, Graduate  
School of Agriculture; 6-10-1, Hakozaki, Higashi-ku, Fukuoka,  
Fukuoka, 812-8581, Japan (E-mail:ohgushi@brs.kyushu-u.ac.jp,  
Tel:81-92-642-3028, Fax:81-92-642-3028)

Location/Qualifiers  
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CDS







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| CDS | /gene="pBt005"<br>complement(4634. .5275)<br>/gene="pBt005"<br>/note="Similar to N-terminus of Bacillus anthracis pxol-18<br>TR:Q9X2Y9 (EMBL:AF065404) (315 aa) fasta scores: E():<br>4.2e-56, 84.15% id in 183 aa, and to Bacillus halodurans<br>Bh2364 protein TR:Q9KAC5 (EMBL:AP001515) (378 aa) fasta<br>scores: E(): 1.6e-18, 35.45% id in 189 aa, and weakly to<br>Lactobacillus delbrueckii integrase/recombinase orf2<br>TR:Q48538 (EMBL:Z50864) (333 aa) fasta scores: E(): 6.3,<br>28.88% id in 90 aa, and to Bacillus thuringiensis<br>resolvase tnpI SW:TNRI_BACTU (P10020) (284 aa) fasta<br>scores: E(): 8.5, 23.88% id in 180 aa"<br>/codon_start=1<br>/transl_table=11<br>/product="integrase/recombinase family protein"<br>/protein_id="CAD30067.1"<br>/db_xref="GI:21685414"<br>/db_xref="GOA:Q8KNX3"<br>/db_xref="InterPro:IPR004107"<br>/db_xref="UniProt/TREMBL:Q8KNX3"<br>/translation="MSKNIINLEETLAFAVSALYIEKGRKQSTIKRYAVDIKDFYKWLRA<br>NKKLHIKSWLSBADYQYFSELEDKRKYKSRHRIWVVLKLMFLCLVSPLDG<br>INLSLIPQSLNDNDFITEEMEKLLKQTVLSTKGLTERQAKYRPLIMDRNVCILNV<br>NYGLSLEQVLSLWNSHINFARNWCYVKKIDILNRDILFVKQLEIVAFHRTSF"<br>complement(4985. .5251)<br>/gene="pBt005"<br>/note="HMPfam hit to PF02899, Phage integrase, N-terminal<br>SAM-like domain"<br>complement(5283. .5286)<br>complement(5364. .5507)<br>/gene="pBt006"<br>complement(5364. .5507)<br>/gene="pBt006"<br>/note="Similar to Bacillus anthracis pxol-17 TR:Q9X2Y8<br>(EMBL:AF065404) (47 aa) fasta scores: E(): 2.1e-12, 68.08%<br>id in 47 aa"<br>/codon_start=1<br>/transl_table=11<br>/product="putative integral membrane protein"<br>/protein_id="CAD30068.1"<br>/db_xref="GI:21685415"<br>/db_xref="UniProt/TREMBL:Q8KNX2"<br>/translation="MAVLKDSNYIEMTYNEIGFGIFWGLIFVVPFWSIMIAPIFW<br>LCK"<br>complement(5370. .5435)<br>/gene="pBt006"<br>/note="1 probable transmembrane helix predicted for pBt006<br>by TMHMM2.0"<br>complement(5515. .5519)<br>complement(6451. .8160)<br>/gene="pBt007"<br>complement(6451. .8160)<br>/gene="pBt007"<br>/note="Similar to Bacillus anthracis pxol-16 TR:Q9X2Y7<br>(EMBL:AF065404) (569 aa) fasta scores: E(): 0.96.13% id<br>in 569 aa, and to Bacillus thuringiensis pxol orf16-like<br>protein TR:CAC50562 (EMBL:AJ296638) (310 aa) fasta scores:<br>E(): 6.5e-122, 99.67% id in 310 aa"<br>/codon_start=1<br>/transl_table=11<br>/product="conserved hypothetical protein"<br>/protein_id="CAD30069.1"<br>/db_xref="GI:21685416"<br>/db_xref="UniProt/TREMBL:Q8KNX1"<br>/translation="MGKSFIIQNSRLNGKTTNAVVTLLKSWQKFAVAFPEKYSYKD<br>TYLEDILOHMTYERADVEGFVEKAPSPFSRRAMSTLAEKTRGKHLXGINTNADLEV<br>FLYLHKCFTNGVI PNVTIMHWEDYKQYKEEFAYIQHSQFYIALKKLNLHNIISTEN<br>GLGRYTIKLTHFMNTEKXNPVVISPVIFTKDFKLSIAKKLFLDIAHQOHTET<br>TLKRSLLDQDERGNKTHFGMYRFLHKVPHQIRAVIELTALPCTGNPLPKCKMQ<br>KGVKTRTYTLYLSIHSDFLSCKEAGEQRDPPTPKATYARKAKFIIVAVLQENNIG<br>ELSDAMNKFIVHLKYTCHQIRSVIRGLRMDVRKEGYPTKIVYTLKLLHOTSOYQI<br>LDTAAKEGIVFLPIAQHIKERNSDREQAVENFGLHYSMTYSLHNIKRMFKNVHALLKQK |  |  |
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LOCUS C0868324 2145 bp DNA linear PAT 13-SEP-2004  
DEFINITION Sequence 25 from Patent WO2004074462.  
ACCESSION C0868324  
VERSION C0868324.1 GI:51998370  
KEYWORDS Bacillus thuringiensis  
SOURCE Bacillus thuringiensis  
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 Carozzi, N., Hargiss, T., Koziel, M.G., Duck, N.B. and Carr, B.  
AUTHORS Delta-endotoxin genes and methods for their use  
TITLE Patent: WO 2004074462-A 25 02-SEP-2004;  
JOURNAL Athenix Corporation (US)  
FEATURES  
source 1..2145  
/organism="Bacillus thuringiensis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:1428"  
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Query Match 14.38; Score 855; DB 6; Length 2145;  
Best Local Similarity 71.44; Pred. No. 3.2e-131;  
Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;  
QY 49 AAATAATGGGTATTATTTGTAGAACATTTGTTACAGGAATACATTTGGGGTACTACGAATAT 108  
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QY 109 ATAGAAAGACACCTAACATATATTTATAGGTGTCTTTAAATAAAGACTATATAAGGAG 168  
DB 68 ATAGAAAGACACCTGGCATATATTTATAGGTGTCTTTAAATAAAGACTATATAAGGAG 127  
QY 169 TGAARAAGATGAGTCCATATCAAAATAAATGAATATGAATATTTGGAATCCTCATCGA 228  
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QY 229 ATACACAAATACCCAAACAGATATCTTTTGCAAATATCGGGATATCTTACTATGT 288  
DB 188 ATACACAAATATGTCAACAGATATCTTTTGCAAAGGATCCAAATATATTTCTTATTA 247  
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DB 308 TAACTATTGGGACATACCTTATACAAATTTCTTGTAGAACCCGGTATAGGTGGAAATTCCTG 367  
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QY 469 CTATATGTGATTTATTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTATG 528  
DB 428 CTATATGTGATTTAGTATCTATAATTCGTAAGAGGTAGACGAGCGTGTAAAGTGACG 487  
QY 529 CGATTGAGATTTTACGGTAAATTTGAAATTTATAGAGATATATCTTTCTTATCTTG 588  
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DB 548 AGAATGGCTTACG-----ATAATCAATCTCAAAACTTGTGACG 592  
QY 649 TAGTTTATTTTAACTTTTCAGAAAGATTTCAATGAAATTTCTAGAGGGTCAATGT 708  
DB 593 TAGTTAAACAGTTTCCAGACGCGGAAGAGATTTCACTAACTTTTAGCAGGCTCATAT 652  
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DB 653 CAAGACAGAAAGCTGAAATATTTATTTGCTACGTATGTGCAAGCTGCAATGTGCAAT 712

QY 769 TATTACTATTAAAGGATCGAGTTTCAATATAAAGCAACATGGTTCCCATTTTGGATCGAG 828  
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DB 773 TGTATCCAGGTCAGGAGAA-----CTGATTGTA 802  
QY 889 ATGAGCGATTAATAATGCAAAACGGCAGAGATATACCAATTTATTTTATATTTGTTATCAGG 948  
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QY 949 TAGGTTTAAATCAGATAAACAACGCGGGACAGGTGCTGACACTTGTGTCGAAATTTAATA 1008  
DB 863 AGGTTTATAGTACAGATAAGACAGCGCGGTACAAGTCTGAAGTTTGTGTCGAAATTTAATA 922  
QY 1009 AATTTCTGATAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTATG 1068  
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DB 1097 CGGTAGAACAAATGGAACAACGCGGACCTGGTTTACTTGGCTTAGCAAGCTATAGATA 1156  
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QY 1300 ATTATGAAGACTACACAAAGGGTAAAGCTATTTTCAACGATGCTCGGAACCTACAGATA 1359  
DB 1217 ATTATGAAGACTTACAAAGGGTAAAGCTTTTCAACGATGCTCTGGAACTACAGATA 1276  
QY 1360 ATGATCTAGCTAATATTGATTTTTCAGAAATCCGAGATATATAAATTTACTTCAATAGCTA 1419  
DB 1277 ATAATCCAGTAAATATTTTGGCAATACCGATATATTTAAATTTATTTCAATAGCTA 1336  
QY 1420 TCATG---AACCTAGTAGAGAGACTACCGCTAGACAGATATCGTGTTCAGAGCGAG 1476  
DB 1337 GATATCAATGCAACCGTTTGTGGGTATTTCAATCCACGGCATCTTTGTTCACTGTCAG 1396  
QY 1477 ATTTTCGTAGGGTAGGGGACCTGATTTAAATTTATGATCGAGTAAATATATGGGCTAAGCA 1536  
DB 1397 AATTTTTCGACACACATTAATACCTTCTGTATGAGGTAAACAGTCTCTGGGTA---CT 1453  
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DB 1514 ATTACTCTCATAGATTTCAATCGGCAATGTTGTTCAGAAATGAAACCTCAGAGTTTAAAG 1573  
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QY 1711 CACAAATACCGGCGGTGAAGAGTTTATCTCTTCAAAATTTATCTTGTAAATGCTTATACCT 1770  
DB 1634 CGCAATCTCTCGATTAAGCTTTTGGCTTACCAGCAGGTACAGGATATGCGAGGAGTT 1693  
QY 1771 ATGTAATAAAGCACT 1787  
DB 1694 ACCTCAGCTGGGCT 1710

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|----------------------------|---|
| RESULT 15                  |   |
| BACISRH3                   |   |
| LOCUS                      | 4186 bp DNA linear BCT 17-FEB-1998  |
| DEFINITION                 | Bacillus thuringiensis israelensis plasmid gene for 130 kDa insecticidal protein (ISRH3), complete cds.   |
| ACCESSION                  | D00247  |
| VERSION                    | D00247.1 GI:216287  |
| SOURCE                     | 130 kDa insecticidal protein (ISRH3).   |
| KEYWORDS                   | Bacillus thuringiensis serovar israelensis  |
| ORGANISM                   | Bacillus thuringiensis serovar israelensis<br>Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.   |
| REFERENCE                  | 1 (bases 1 to 4186)   |
| AUTHORS                    | Sen,K., Honda,G., Koyama,N., Nishida,M., Neki,A., Sakai,H., Himeno,M. and Komano,T.   |
| TITLE                      | Cloning and nucleotide sequences of the two 130 kDa insecticidal protein genes of Bacillus thuringiensis var. israelensis   |
| JOURNAL                    | Agric. Biol. Chem. 52, 873-878 (1988)   |
| COMMENT                    | The genes of ISRH3 and ISRH4 that were 130 kDa insecticidalu proteins of Bti were sequenced and compared with other insecticidal protein genes. ISRH3 and ISRH4 were identical in a region of the C-terminal 467 amino acids.   |
| FEATURES                   | Location/Qualifiers   |
| source                     | 1..4186   |
|                            | /organism="Bacillus thuringiensis serovar israelensis"  |
|                            | /mol_type="genomic DNA"   |
|                            | /strain="HD522"   |
|                            | /sub_species="israelensis"  |
|                            | /db_xref="taxon:1430"   |
|                            | /clone="pBGH3"  |
|                            | /plasmid="pBti-5 and pBti-6"  |
|                            | /notes="Clal site"  |
|                            | 449..453  |
| RBS                        | /notes="Shine-Dalgarno sequence"  |
| CDS                        | 461..3868   |
|                            | /codon_start=1  |
|                            | /transl_table=11  |
|                            | /product="130 kDa insecticidal protein (ISRH3)"   |
|                            | /protein_id="BAA00178.1"  |
|                            | /db_xref="GI:216288"  |
|                            | /translation="MNSGYPLANDLOGSMKNTNYKDWLAWCENNOQYGVNPAAINSSD VSTLAKVAILKFNVPAGTVLTVLSAVLPILPNTPTPERVNDPMTNGLIDQ TTVAYVRTANAKMTVVDYLDQYTKFNWKREPNQSYRTAVTQFNLTSAKURET AVFSNLVGEILLPLPIYAQVANFNLLIRDGLINAQEWSLACAGDLVNTWVYKKE IYASHITWYKGLDVLNRKNSGOWITFNDYKREMTIQVILDILAFASYDPRLPADKI DNTKLSKTFREIYALVESPSKSI AALEALTRDVLHLTKRVYFWPTNPIQDL RFLSANKIFSNTSAGMOESGIYSGSGFSGNLTHQIOLNSVYKTSI TDTSSPSNRV TMDRFVKGIDTLASVNSITPTPEGLRTTFRGSTNENTPNQPTVNDVYTHILSYKTD VIDNSNRVSPAWTHKIVDPNQIYTDALITQVPAVKSFNLTAKVIKPGHTGGDLV ALTSNGLSGRMEIOCKTSIFNDPFRSYGLRIYAAANSPIVLNVSVLQGVSRGFTIS TESTFRPNIIPTDLKYEFRYKDPDAIVPMRLSSNQLITAIQPLNMTSNNOVII DRIEITPTQSVLDEPENONLESEREVNALFTNDAKDALNIGTDDYDIDQANLVEE ISEELYPKEMLLDVBKNAKOLQSQRNVLONGDRSALTGWTSNITIDRDDPIFEK GHYLMHSGARDIDGTTFPTVYIQKIDESKLPYTRYLVYVGFVSGSKDVELVYRVEE IDAINVNPADLNYLYPSTDCGSRNCRSETSAPVANGNTSDMLSCQYDTGKRVVCQ DSHQSFDTIDGALDINENIWMVMPKISSPDGYASLDNLLEVI BEGPIDEALSRVKH MEKWNDOEAKRSETQOAYDYAKQIDALFTNVQDEALQFDPTLLAQIYAEYLVQSI PYYVNDLSDVPMYDIYVELDARVAQARYLYIDRNIIKNGDFTQGVMGVHWIYNAD VQOIDGVSVLVNWSAGVSNVHLQHNHGYLVRLIAKKEGPGNGVYVTLDCENQEK LFTSCSEGYIITKVDVFPDTRVRIEIGETSGSFYIESIELICMNE" |
| ORIGIN                     |   |
| Query Match                | 13.2%; Score 790.6; DB 1; Length 4186;  |
| Best Local Similarity      | 67.5%; Pred. No. 1.1e-120;  |
| Matches 1184; Conservative | 0; Mismatches 539; Indels 30; Gaps 4;   |
| Qy                         | 2260 TTCTACTAGATAGTGGTATTGCTGTTTAAACAATAAGCGAAAAAGGTTGTGAGTCCTAT 2319   |
| Db                         | 2365 TGTATTAGATGACAGACAGAACCAAAATTTAGATACTCAGAACGAGAAATGTTGTAATGCAT 2424  |
| Qy                         | 2320 GTTTACAAGTAGTACGAAAAATACGTTTAAAAATAGAAAAACACACAGATTATGAATAGATCA 2379   |
| Db                         | 2425 GTTTACAAATGACCGCGAAGATGCATTAAACATTTGGNACGACAGATTATGACATAGATCA 2484   |



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| Result No. | Score | Query | ID   | DB | Length   | Match | Description         |
|------------|-------|-------|------|----|----------|-------|---------------------|
| 1          | 126.6 | 2.1   | 2711 | 9  | BH771014 |       | BH771014 LLMGtag73  |
| 2          | 77.6  | 1.3   | 471  | 10 | CG807194 |       | CG807194 1118078H0  |
| 3          | 75.8  | 1.3   | 1101 | 10 | CNS0039G |       | AL063921 Drocephill |
| 4          | 73.2  | 1.2   | 429  | 10 | CG803197 |       | CG803197 1118039H0  |
| 5          | 71.2  | 1.2   | 363  | 10 | CG807311 |       | CG807311 1118080F0  |
| 6          | 70    | 1.2   | 670  | 9  | B388480  |       | B388480 EIND211TF   |
| 7          | 69.6  | 1.2   | 580  | 11 | CR479976 |       | CR479976 mth2-190L  |
| 8          | 69.6  | 1.2   | 685  | 10 | CG937658 |       | CG937658 MBEBE62TR  |
| 9          | 69.6  | 1.2   | 891  | 10 | CG937914 |       | CG937914 MBEH073TR  |
| 10         | 68.6  | 1.1   | 379  | 10 | CG807081 |       | CG807081 1118077E0  |
| 11         | 68.2  | 1.1   | 832  | 9  | BH391984 |       | BH391984 AG-ND-138  |
| 12         | 68    | 1.1   | 735  | 10 | CW960936 |       | CW960936 A1AA-aac1  |
| 13         | 67.8  | 1.1   | 398  | 9  | A2935561 |       | A2935561 M028 E. c  |
| 14         | 67.6  | 1.1   | 302  | 10 | CG807096 |       | CG807096 1118077G0  |
| 15         | 67    | 1.1   | 679  | 4  | AY066713 |       | AY066713 Schmdtea   |
| 16         | 66.4  | 1.1   | 400  | 10 | CG807323 |       | CG807323 1118080G0  |
| 17         | 66.4  | 1.1   | 430  | 10 | CG803196 |       | CG803196 1118039H0  |
| 18         | 66.4  | 1.1   | 889  | 10 | CW973509 |       | CW973509 A1AA-aaas  |
| 19         | 66.2  | 1.1   | 518  | 10 | CG086559 |       | CG086559 PUQC11TD   |
| 20         | 66.2  | 1.1   | 891  | 10 | CW952279 |       | CW952279 TcB38.1.B  |
| 21         | 65.6  | 1.1   | 707  | 10 | CW187604 |       | CW187604 104_607.1  |
| 22         | 65.2  | 1.1   | 736  | 9  | CQ077693 |       | CQ077693 CSU-K33r-  |



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
(bases 1 to 425)  
Walbot, genomic sequences found using engineered Rescuemu transposon  
Unpublished (2001)  
Contact: walbot.v

Contact: Walbot V  
Department of Biological Sciences

```

standord University
855 University Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1118039 row: 2
Class: transposon-tagged.
Location/Qualifiers
1. .429
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

## ORIGIN

|    | Query Match  | 1.2%; Score 73.2; DB 10; Length 429; |
|----|--|--------------------------------------|
|    | Best Local Similarity 51.6%; Pred. No. 4e-05;                              |                                      |
|    | Matches 191; Conservative 0; Mismatches 178; Indels 1; Gaps 1;             |                                      |
| Qy | 3762 ATGATACAAATAATAACCTGCACACGGGTAAATATGTATGAGCAAGATTATAATGGAAATT 3821    |                                      |
| Db | 35 ATAATAATAATAATAATAATATTAATAATTAATTAATAATATTAATAATAATAATA 94             |                                      |
| Qy | 3822 ATAATCAAAATACTAGCGATGTGTATTACCAAGGGTATACAAACAACACTATAACCAAGACT 3881   |                                      |
| Db | 95 ATAATAATAATATTATTTATAATAATAATAATAATTAATAATAATAATAATAATAATT 154          |                                      |
| Qy | 3882 CTAGTAAATGTATAATCAAAATTTACTTAACAATGATGACCTTCGGTGGCAT 3941             |                                      |
| Db | 155 ATAGTTATAATTATAATTATTTATAATAATAATAATTAATAATTAATAATAATAATA 214          |                                      |
| Qy | 3942 GTAACCAAGGGCATAACTCTGGCTGTACATGTAAATCAAGGATATAACCGTTA-ACGATTC 4000    |                                      |
| Db | 215 ATAATAAATTTATAATAATAATAATTTATAATTAATAATAATAATAATAATAATAATA 274         |                                      |
| Qy | 4001 TAAATAAGAATCAACATCATTTGGCAAAATAAATAAACCCTACTCAAAAATCTATTGGCATAT 4060  |                                      |
| Db | 275 ATAATAATAATAATAATAATAATAATGATAAATAATAATAATAATAATAATAATAATAATA 334      |                                      |
| Qy | 4061 CATAAACATAGCTTTTACAAAATAACGGACATATTCTAGAGAGAGGTCTCCTTAATTCATAAAA 4120 |                                      |
| Db | 335 ATA 394       |                                      |
| Qy | 4121 TAAGGAGATT 4130   |                                      |
| Db | 395 TAATTATAAT 404   |                                      |

|            |   |             |     |        |                 |
|------------|---|-------------|-----|--------|-----------------|
| RESULT 4   | CG803197  | 429 bp      | DNA | linear | GSS 10-NOV-2003 |
| LOCUS      | CG803197  |             |     |        |                 |
| DEFINITION | 1118039H04.Y1 l118 - RescueMu Grid S Zea mays genomic, genomic survey sequence. |             |     |        |                 |
| ACCESSION  | CG803197  |             |     |        |                 |
| VERSION    | CG803197.1  | GI:38238983 |     |        |                 |
| KEYWORDS   | GSS.  |             |     |        |                 |
| SOURCE     | Zea mays  |             |     |        |                 |
| ORGANISM   | Zea mays  |             |     |        |                 |

|            |   |             |     |        |                 |
|------------|---|-------------|-----|--------|-----------------|
| RESULT 4   | CG803197  | 429 bp      | DNA | linear | GSS 10-NOV-2003 |
| LOCUS      | CG803197  |             |     |        |                 |
| DEFINITION | 1118039H04.Y1 l118 - RescueMu Grid S Zea mays genomic, genomic survey sequence. |             |     |        |                 |
| ACCESSION  | CG803197  |             |     |        |                 |
| VERSION    | CG803197.1  | GI:38238983 |     |        |                 |
| KEYWORDS   | GSS.  |             |     |        |                 |
| SOURCE     | Zea mays  |             |     |        |                 |
| ORGANISM   | Zea mays  |             |     |        |                 |

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RESULT 5
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LOCUS      1118080F01.y1 1118 - RescueMu Grid S Zea mays genomic, linear GSS 10-NOV-2003
DEFINITION survey sequence.
ACCESSION  CG807311
VERSION     CG807311.1 GI:38244939
KEYWORDS   Zea mays
SOURCE      Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 363)
            Walbot,V.
            Maize genomic sequences found using engineered RescueMu transposon
            Unpublished (2001)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1118080 column: 3
            Class: transposon-tagged.
            Location/Qualifiers
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                /organism="Zea mays"
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                /db_xref="taxon:4577"
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                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="1118 - RescueMu Grid S"
                /notes="Organ: leaf; Vector: RescueMu (engineered from
                pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescueMu, go to the web
                site 'www.zmdb.iastate.edu' and follow the links for
                'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
                extracted from leaf strips, double digested using BamHI
                and BglII, and ligated to form circular plasmids. DH10B
                cells were transformed and then screened on LB plates with
                ampicillin."
FEATURES
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        1..363
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /note="Vector: phos2; Site_1: BstXI; Total genomic DNA was
        isolated from early log phase trophozoites of E. invadens
        IP-1 using a Qiagen plant DNA extraction kit. A shotgun
        medium-size plasmid library (average insert size of 10 -
        12 kb) was generated by random mechanical shearing of E.
        invadens genomic DNA, repairing the ends of DNA fragments
        with T4 Polymerase, adding BstXI adaptors and ligating
        into the BstXI site of a pUC-derived vector phos2."
ORIGIN
    Query Match      1.2%; Score 71.2; DB 10; Length 363;
    Best Local Similarity 51.4%; Pred. No. 0.00011;
    Matches 163; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
    QY 3718 TACATTTTATAGATGACATCGAGTTGCTTTGTATGCGAAGATATGATAACAATATAA 3777
    Db 47 TAATANTTATAATAATTTATAATAATAATAATAATAATAATAATAATAATAATAATATAT 106
    QY 3778 CCTGCACACGGGTAATATGTATGACGCAAGTTTAAATGGAATTTATAATCAAAATACTAG 3837
    Db 107 TTATAATTATCTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 166
    QY 3838 CGATGTGTATTACCAAGGGTATACAAACACTATAACCAAGACTCTAGTAATATGTATAA 3897
    Db 167 TAATAATTATAATAATAATTATATAATAATAATAATAATAATAATAATAATAATAATAATA 226
    QY 3898 TCAGAAATTATACAAAGATGACCTGCATTCGGTTGACATGTAAACCAAGGGCATAA 3957
    Db 227 TAATAATTATAATAATAGTTATATAATAATAATAATAATAATAATAATAATAATAATCATAC 286
    QY 3958 CTCTGCTGTACATGTGAATCAAGGATATAACCGTTAACGATTTCTAAATAAGATCAACAT 4017
    Db 287 TAATAATTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 346
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QY 4018 CATTGCGAAATAATAAA 4034
Db 347 TAATAATAATAATAATA 363

RESULT 6
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LOCUS      EINDL21TF EI_10_12_KB Entamoeba invadens genomic clone EINDL21,
DEFINITION genomic survey sequence.
ACCESSION  BZ388480
VERSION     BZ388480.1 GI:30235017
KEYWORDS   GSS.
SOURCE      Entamoeba invadens
ORGANISM   Entamoeba invadens
            Eukaryota; Entamoebidae; Entamoeba.
            1 (bases 1 to 670)
            Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van
            Dellen,K., Hall,N., Anderson,I. and Loftus,B.
            Gene discovery in the Entamoeba invadens genome
            Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
            12798503
            Other_GSSs: EINDL21TR
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: entae@tigr.org
            DNA was provided by Daniel Eichinger
            Seq primer: TF
            Class: sheared ends.
FEATURES
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        1..670
        /organism="Entamoeba invadens"
        /mol_type="genomic DNA"
        /strains="IP-1"
        /db_xref="taxon:33085"
        /clone_lib="EINDL21"
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        /note="Vector: phos2; Site_1: BstXI; Total genomic DNA was
        isolated from early log phase trophozoites of E. invadens
        IP-1 using a Qiagen plant DNA extraction kit. A shotgun
        medium-size plasmid library (average insert size of 10 -
        12 kb) was generated by random mechanical shearing of E.
        invadens genomic DNA, repairing the ends of DNA fragments
        with T4 Polymerase, adding BstXI adaptors and ligating
        into the BstXI site of a pUC-derived vector phos2."
ORIGIN
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    Best Local Similarity 49.2%; Pred. No. 0.00023;
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    QY 3762 ATGATAACAATAAATACCTGCACACGGGTAATATGTATGAGCAAAAGTTATATGGAAT 3821
    Db 603 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 544
    QY 3822 ATAATCAAAATACTAGCGATGTATTACCAAGGGTATACAAACACTATATACCAAGACT 3881
    Db 543 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 484
    QY 3882 CTAGTAATATGTATTAATCAAAATTAATCTAACAATGATGACCTGCATTCGGTTGCACAT 3941
    Db 483 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 424
    QY 3942 GTAAACCAAGGGCATAACTCTGCTGTACATGTAAATCAAGGATATACCGTTAACGATTCT 4001
    Db 423 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 364
    QY 4002 AAATAAGATCAACATCATCTGCGAAAAATAAAAAACCTACTCAGAAAACTATTGTCATATC 4061
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AG-ND-138G17, genomic survey sequence.
BH391984
VERSION BH391984.1 GI:17338125
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
REFERENCE Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
AUTHORS Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 832)
Hong,Y.S., Hogan,J.R., Wang,X., Sarkar,A., Sim,C., Loftus,B.J.,
Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B.,
Gardner,M.J. and Collins,F.H.
TITLE Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae
JOURNAL Mal. Genet. Genomics 268 (6), 720-728 (2003)
PUBMED 12655398
COMMENT Other GSSs: AG-ND-138G17.TF.1
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
(DNA). All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 Rev
Class: BAC ends.
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     /note="Vector: pECBAC1; Site_1: HindIII"
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QY 3747 TTGTATGCAGGATATGATAACAATAATAAAGCTGCACACGGGTATATGTATGACAAA 3806
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QY 3807 GTTATATGGAATTTATATCAAAATCTAGCGATGTATTACCAAGGGTATACAAACA 3866
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DB 409 ATAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 468
QY 3867 ACTATAACCAAGACTCTAGTAAATATGTATAATCAAAATTTATCTAAATATGACCTGC 3926
    |||||
DB 469 ATAATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 528
QY 3927 ATTCCGGTTCACATGTAACCAAGGCGATAACTCTCGGCTGTACATGTATCAAGGATATA 3986
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DB 529 ATAATGATAGTAAAAATCATATAATAATGATAATAATAATAATAATAATAATAATAATA 588
QY 3987 ACCGTTTAACGATTTCTAAATAAGAAATCAACATCATTCGCGAATAATAAAACCTACTCACA 4046
    |||||
DB 589 AATAATAATAATAAAT-AAATAATAGTAATAATAATAATAATAATAATAATAATAATAATA 647
QY 4047 AATCTATTGCATATCATATAAGCTTTTACAATAAACCAGACATATTCTTAGAAGAGGTCT 4106

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Db 648 AATAATAATAATAATAATAATAATAATTCATATCATATATAATAATAATAATAATAA 707
QY 4107 CCTTAATTCCTAAATAAGGAGATTTTTT 4135
Db 708 TATTTATTAATAATAATAATAAAGTATTTT 736

RESULT 12
LOCUS CW960936
DEFINITION AIAA-aac14d08.b1 Ancylostoma caninum whole genome shotgun library
(AIAAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION CW960936
VERSION CW960936.1 GI:56761663
KEYWORDS GSS.
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Ancylostoma caninum
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
AUTHORS Ancylostomatidae; Ancylostomatidae; Ancylostoma.
1 (bases 1 to 735)
Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R.,
Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
Waterston,R.H., Clifton,S.W. and Wilson,R.
TITLE Genome Survey sequences from the parasitic nematode Ancylostoma
caninum
JOURNAL Unpublished (2004)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon (mtmjmh@wumc.edu) DNA
sequenced by Washington University Genome Sequencing Center
Class: shotgun.
FEATURES             Location/Qualifiers
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     strain="Baltimore"
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     /note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI;
     Ancylostoma caninum genomic DNA was randomly sheared,
     end-repaired and size fractionated to enrich for 2-4 kb
     fragments. Genomic DNA was provided by John Hawdon
     (mtmjmh@wumc.edu) at George Washington University.
     Sequencing by Washington University Genome Sequencing
     Center, St. Louis, MO."
ORIGIN
Query Match          1.1%; Score 68; DB 10; Length 735;
Best Local Similarity 50.3%; Pred. No. 0.00064;
Matches 167; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
QY 3762 ATGATAACAATAATAACCTGCACACGGGTAATATGTATGACGAAAGTTATTAATGGAATT 3821
    |||||
DB 224 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 283
QY 3822 ATAATCAAAATACTACGGATGTATTACCAAGGGTATACAACTACTAACCAAGACT 3881
    |||||
DB 284 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 343
QY 3882 CTAGTAATAATGTATAATCAAAATTTACTACCAAGATGACCTGCATTCGGTGGACAT 3941
    |||||
DB 344 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 403
QY 3942 GTAACCAAGGGCATAACTCTGCTGTACATGTAAATCAAGGATATAACCGTTACGATTCT 4001

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 09:48:39 ; Search time 2211.9 Seconds  
(without alignments)  
18018.361 Million cell updates/sec

Title: US-10-781-979-1

Perfect score: 5980

Sequence: 1 tacatgaataacataaagag.....ttctaaaaagcctctgtat 5980

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004as.\*  
13: Geneseq2004bs.\*  
14: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 5980  | 100.0       | 5980   | 13 ADR89400 | Adr89400 AXMI-008  |
| 2          | 2082  | 34.8        | 2082   | 13 ADR89401 | Adr89401 AXMI-008  |
| 3          | 2073  | 34.7        | 2073   | 13 ADR89403 | Adr89403 AXMI-008  |
| 4          | 1686  | 28.2        | 1686   | 13 ADR89405 | Adr89405 AXMI-008  |
| 5          | 967   | 16.2        | 4391   | 14 AEA61394 | Aea61394 Bacillus  |
| 6          | 855   | 14.3        | 2145   | 13 ADR89413 | Adr89413 AXMI-008  |
| 7          | 790.6 | 13.2        | 3684   | 1 AAN82106  | Aan82106 Sequence  |
| 8          | 789   | 13.2        | 3684   | 6 ABK14949  | Abk14949 Bacillus  |
| 9          | 789   | 13.2        | 3684   | 14 AEA61392 | Aea61392 Bacillus  |
| 10         | 789   | 13.2        | 4065   | 1 AAN92515  | Aan92515 Sequence  |
| 11         | 787.4 | 13.2        | 3535   | 1 AAN91003  | Aan91003 Sequence  |
| 12         | 781.8 | 13.1        | 4184   | 1 AAN96139  | Aan96139 Bacillus  |
| 13         | 774.6 | 13.0        | 4934   | 1 AAN81490  | Aan81490 Insectici |
| 14         | 765.8 | 12.8        | 3543   | 2 AAO81178  | Aao81178 B.t. toxi |
| 15         | 764.2 | 12.8        | 3543   | 2 AAO81178  | Aao81178 B.t. toxi |
| 16         | 747.2 | 12.5        | 2019   | 13 ADR89414 | Adr89414 AXMI-008  |
| 17         | 739.8 | 12.4        | 2019   | 13 ADR89416 | Adr89416 AXMI-008  |
| 18         | 714   | 11.9        | 10974  | 1 AAN60055  | Aan60055 VB131 clo |
| 19         | 639.8 | 10.7        | 4571   | 1 AAN93059  | Aan93059 Delta-end |

|    |       |     |      |             |                    |
|----|-------|-----|------|-------------|--------------------|
| 20 | 450.6 | 7.5 | 3940 | 1 AAN93054  | Aan93054 Delta-end |
| 21 | 402   | 6.7 | 3756 | 1 AAN50525  | Aan50525 Bacillus  |
| 22 | 390   | 6.5 | 4359 | 8 ABX13486  | Abx13486 B. popill |
| 23 | 390   | 6.5 | 4359 | 14 AEB90814 | Aeb90814 Paenibaci |
| 24 | 380.8 | 6.4 | 3690 | 6 ABK51132  | Abk51132 cDNA enco |
| 25 | 358   | 6.0 | 3797 | 2 AAO36866  | Aao36866 Coleopter |
| 26 | 358   | 6.0 | 3797 | 2 AAO58975  | Aao58975 B.thuring |
| 27 | 318.6 | 5.3 | 4366 | 8 ABX13497  | Abx13497 B. popill |
| 28 | 318.6 | 5.3 | 4366 | 14 AEB90830 | Aeb90830 Paenibaci |
| 29 | 317.8 | 5.3 | 3471 | 2 AAO51704  | Aao51704 Bacillus  |
| 30 | 314.6 | 5.3 | 3471 | 2 AAO30821  | Aao30821 Toxin 50C |
| 31 | 314.6 | 5.3 | 3471 | 2 AAO27167  | Aao27167 Delta-end |
| 32 | 314.6 | 5.3 | 3471 | 2 AAO28940  | Aao28940 B.thuring |
| 33 | 314.6 | 5.3 | 3471 | 2 AAO38653  | Aao38653 Bt isolat |
| 34 | 314.6 | 5.3 | 3471 | 2 AAO38653  | Aao38653 Bt isolat |
| 35 | 313   | 5.2 | 4896 | 6 AAD43974  | Aad43974 Antiscara |
| 36 | 313   | 5.2 | 4896 | 10 ADF31301 | Adf31301 Bacillus  |
| 37 | 313   | 5.2 | 4896 | 10 ADF31306 | Adf31306 Bacillus  |
| 38 | 312.2 | 5.2 | 4359 | 8 ABX13496  | Abx13496 B. popill |
| 39 | 312.2 | 5.2 | 4359 | 14 AEB90828 | Aeb90828 Paenibaci |
| 40 | 310.4 | 5.2 | 6930 | 6 AAD43973  | Aad43973 Bacillus  |
| 41 | 310.4 | 5.2 | 6930 | 10 ADF31299 | Adf31299 Bacillus  |
| 42 | 310.4 | 5.2 | 6930 | 10 ADF31304 | Adf31304 Bacillus  |
| 43 | 308.6 | 5.2 | 4004 | 2 AAO05680  | Aao05680 btPGS1245 |
| 44 | 308.2 | 5.2 | 4188 | 8 ABX13487  | Abx13487 B. popill |
| 45 | 308.2 | 5.2 | 4188 | 14 AEB90816 | Aeb90816 Paenibaci |

## ALIGNMENTS

### RESULT 1

ADR89400

ID ADR89400 standard; cDNA; 5980 BP.

XX AC ADR89400;

DT 18-NOV-2004 (first entry)

DE AXMI-008 full length coding sequence.

XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;

KW expression cassette; transformation; transgenic; plant; bacteria;

KW lepidoptera; coleoptera; pest; pesticide; resistance;

KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers

FT CDS 188..2249

FT /\*tag= a

FT /product= "AXMI-008"

FT /transl\_except= pos:168..170, aa:Met

XX WO2004074462-A2.

PN 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

PR 20-FEB-2003; 2003US-0448632P.

PR 20-FEB-2003; 2003US-0448633P.

PR 20-FEB-2003; 2003US-0448797P.

PR 20-FEB-2003; 2003US-0448806P.

PR 20-FEB-2003; 2003US-0448810P.

PR 20-FEB-2003; 2003US-0448812P.

PR 19-FEB-2004; 2004US-00781979.

PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.

PR 19-FEB-2004; 2004US-00782141.

PR 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

PA (ATHE-) ATHENIX CORP.  
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
XX WPI; 2004-635574/61.  
XX P-PSDB; ADR89402.  
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.  
XX  
PS Claim 1; SEQ ID NO 12; 178pp; English.  
XX  
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-  
XX endotoxin coding sequences of the invention have alternative start  
XX codons, producing more than one protein from a single open reading frame.  
XX The nucleic acid sequences of the invention are useful in DNA constructs  
XX or expression cassettes for transformation and expression in plants and  
XX bacteria. The nucleic acids and corresponding polypeptides are useful for  
XX killing lepidopteran or coleopteran pests. Compositions containing the  
XX delta-endotoxins of the invention, and methods for their production, are  
XX useful for the production of organisms with pesticide resistance,  
XX specifically bacteria and plants. These organisms are useful for  
XX generating altered or improved delta-endotoxin or delta-endotoxin-  
XX associated proteins that have pesticidal activity, or for detecting the  
XX presence of delta-endotoxin or delta-endotoxin-associated proteins or  
XX nucleic acids in products or organisms.  
XX  
SQ Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5980; DB 13; Length 5980;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TACATGCAATACATAAGAGAGAGGTTTAAAAAATCAATACCTCACCACAAAATTAATGGTT 60  
DB 1 TACATGCAATACATAAGAGAGAGGTTTAAAAAATCAATACCTCACCACAAAATTAATGGTT 60  
  
QY 61 TATTGTGAGAAACATTGTTACAGGAATACATTCGGGTACTACGAATATATAGAAAGACAC 120  
DB 61 TATTGTGAGAAACATTGTTACAGGAATACATTCGGGTACTACGAATATATAGAAAGACAC 120  
  
QY 121 CTAACATATATTTAGGTGCTTAAAAATAGGACTATATAGGAGTGAAGAAATGA 180  
DB 121 CTAACATATATTTAGGTGCTTAAAAATAGGACTATATAGGAGTGAAGAAATGA 180  
  
QY 181 GTCATATCAAAATAAAATGAATATGAATATGGAACTCCTCATCGAATAACACAAATA 240  
DB 181 GTCATATCAAAATAAAATGAATATGAATATGGAACTCCTCATCGAATAACACAAATA 240  
  
QY 241 CGCCAAACAGATATCCTTTTGCAATAATCGGGATATGCTACTATGTCTTGGAAATGAT 300  
DB 241 CGCCAAACAGATATCCTTTTGCAATAATCGGGATATGCTACTATGTCTTGGAAATGAT 300  
  
QY 301 GTCAGGGAATCTCATGGGATGAATTTGGGAATCAGTCGAAACGATAACAGTATTGGGA 360  
DB 301 GTCAGGGAATCTCATGGGATGAATTTGGGAATCAGTCGAAACGATAACAGTATTGGGA 360  
  
QY 361 TAAATCTTATAGAGTTTGATAGAACCTAGTTTGGGTGGAAATAAATACACTATTATCAA 420  
DB 361 TAAATCTTATAGAGTTTGATAGAACCTAGTTTGGGTGGAAATAAATACACTATTATCAA 420  
  
QY 421 TAATAGAAACCTAAATTCGACTAAATCGTCAAACTGTGTGAGCACTTTCTATATGAT 480  
DB 421 TAATAGAAACCTAAATTCGACTAAATCGTCAAACTGTGTGAGCACTTTCTATATGAT 480  
  
QY 481 TATTATCTAAATTCGTAAGAGGTAGCCGATAGTCTTTTAAGTGTGCGATTCGAGATT 540  
DB 481 TATTATCTAAATTCGTAAGAGGTAGCCGATAGTCTTTTAAGTGTGCGATTCGAGATT 540  
  
QY 541 TTGACGGTAAATTCGAAATATATAGAGATTTATCTTTCTTATCTTTGGGCTTGGCTTA 600  
DB 541 TTGACGGTAAATTCGAAATATATAGAGATTTATCTTTCTTATCTTTGGGCTTGGCTTA 600

QY 601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGACAAATTTAGTTTATTATT 660  
DB 601 AAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGACAAATTTAGTTTATTATT 660  
  
QY 661 TTTAAACTTTTCAGAAAGAGATTTCAATGAAATCTAGGAGGGTCATTGTCAAGAAACAAATG 720  
DB 661 TTTAAACTTTTCAGAAAGAGATTTCAATGAAATCTAGGAGGGTCATTGTCAAGAAACAAATG 720  
  
QY 721 CTCAAGTATTTGTTATTTACCTACTTTTGACAAAGCTGCAAAATGTGAGTTTATTACTATTAA 780  
DB 721 CTCAAGTATTTGTTATTTACCTACTTTTGACAAAGCTGCAAAATGTGAGTTTATTACTATTAA 780  
  
QY 781 GGGATGCACTTCAATATATAAGCACAAATGGTTCCCAATTTTGTAGTGACAGAAATGTAAGAT 840  
DB 781 GGGATGCACTTCAATATATAAGCACAAATGGTTCCCAATTTTGTAGTGACAGAAATGTAAGAT 840  
  
QY 841 CGGAATTAATATACCTAACAGTGGTTGATTTTACCGGTGATTACTATGAGCGGATTA 900  
DB 841 CGGAATTAATATACCTAACAGTGGTTGATTTTACCGGTGATTACTATGAGCGGATTA 900  
  
QY 901 AATGCAAAACGGCAGAGTATACCAATTTATTTGTTATTTGGTATCAGGTAGGTTTAAATC 960  
DB 901 AATGCAAAACGGCAGAGTATACCAATTTATTTGTTATTTGGTATCAGGTAGGTTTAAATC 960  
  
QY 961 AGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAATAAATTCGTAGAG 1020  
DB 961 AGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAATAAATTCGTAGAG 1020  
  
QY 1021 AAATGACGTTGGCGGTATTGGATATTTATCGCTATATTTCCAACTTATGATTTTGAGAAAT 1080  
DB 1021 AAATGACGTTGGCGGTATTGGATATTTATCGCTATATTTCCAACTTATGATTTTGAGAAAT 1080  
  
QY 1081 ATCCATTTGCAACACATGTAGAGTTGACTAGGGAATTTATACAGATGCAAGTGGGATATT 1140  
DB 1081 ATCCATTTGCAACACATGTAGAGTTGACTAGGGAATTTATACAGATGCAAGTGGGATATT 1140  
  
QY 1141 CATCGGGAACCTTATAGTTGGTTACGGAATGGCCCTAAATCTTTTAAATGGGTTAGAGGCTA 1200  
DB 1141 CATCGGGAACCTTATAGTTGGTTACGGAATGGCCCTAAATCTTTTAAATGGGTTAGAGGCTA 1200  
  
QY 1201 ATGGAACACGGGACCTGGTTTGTAGTTTACCTGCTTAGCAAAATAGTATATATATGAGT 1260  
DB 1201 ATGGAACACGGGACCTGGTTTGTAGTTTACCTGCTTAGCAAAATAGTATATATATGAGT 1260  
  
QY 1261 ATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCATTTATGAAGACTACACAAAG 1320  
DB 1261 ATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACTCGTCATTTATGAAGACTACACAAAG 1320  
  
QY 1321 GTAAACGGTATTTTTCGAACTGCTGGAACCTACGAGTAAATGATCTACGTAATATTGAT 1380  
DB 1321 GTAAACGGTATTTTTCGAACTGCTGGAACCTACGAGTAAATGATCTACGTAATATTGAT 1380  
  
QY 1381 TTTCAAGATCCGATGTATATAAAATTTACTTTCAAGGCGAGATTTTCGTAGGGTAGGGGACCTG 1440  
DB 1381 TTTCAAGATCCGATGTATATAAAATTTACTTTCAAGGCGAGATTTTCGTAGGGTAGGGGACCTG 1440  
  
QY 1441 CTACCGCTAGACACAGATATCGTTTTCGAAAGCGAGATTTTCGTAGGGTAGGGGACCTG 1500  
DB 1441 CTACCGCTAGACACAGATATCGTTTTCGAAAGCGAGATTTTCGTAGGGTAGGGGACCTG 1500  
  
QY 1501 ATTTAAATTTATGATGAGGTAATTAATGGCTAAGCGGATGACAAATTTGAATCTACGCTTC 1560  
DB 1501 ATTTAAATTTATGATGAGGTAATTAATGGCTAAGCGGATGACAAATTTGAATCTACGCTTC 1560  
  
QY 1561 CACTTGTATTTGCACTCTAATGGTTTGTAGAGGACCTCTCCTATAGATTTATCAATTCGGCAT 1620  
DB 1561 CACTTGTATTTGCACTCTAATGGTTTGTAGAGGACCTCTCTCATAGATTTATCAATTCGGCAT 1620  
  
QY 1621 GTGTTGTATATAGGAACTCCAGATTTAAGCTATATGTTTGGACACATACAAGTTTAAAC 1680  
DB 1621 GTGTTGTATATAGGAACTCCAGATTTAAGCTATATGTTTGGACACATACAAGTTTAAAC 1680





Db 3841 TGTGTATTACCAAGGATATACAAACAACTATAACCAAGACTCTAGTAATATGTATTAATCA 3900  
QY 3901 AAATTAATACAAATGATGACCTGCATTCGGGTGCACATGTAAACCAAGGGCATAACTC 3960  
Db 3901 AAATTAATACAAATGATGACCTGCATTCGGGTGCACATGTAAACCAAGGGCATAACTC 3960  
QY 3961 TGGCTGTACATGTAATCAAGGATATAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020  
Db 3961 TGGCTGTACATGTAATCAAGGATATAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020  
QY 4021 TGGCAAAATTAACAACTACTACAAATCTATTTGCATATATATGCAATATATTAAGCTTTTACAAA 4080  
Db 4021 TGGCAAAATTAACAACTACTACAAATCTATTTGCATATATATGCAATATATTAAGCTTTTACAAA 4080  
QY 4081 TAAACGACATATTTCTAGAAAGAGGTCTCTTTAAATTAAGAGATATTTTTCGTTT 4140  
Db 4081 TAAACGACATATTTCTAGAAAGAGGTCTCTTTAAATTAAGAGATATTTTTCGTTT 4140  
QY 4141 CCCCAATATGTAATTAAGAAATACCTCTTTACAGAAAGATTTAGGCTGATTTGGTGTTTT 4200  
Db 4141 CCCCAATATGTAATTAAGAAATACCTCTTTACAGAAAGATTTAGGCTGATTTGGTGTTTT 4200  
QY 4201 GTGCAAGCAGCAATTCCTGAAAATGCAGAAAAATTCAGAGGCATGCAGCTACTTTT 4260  
Db 4201 GTGCAAGCAGCAATTCCTGAAAATGCAGAAAAATTCAGAGGCATGCAGCTACTTTT 4260  
QY 4261 TAAATGTTAAATTTGGTATTTCCAGAAATGATAAGCAATTTCTGTAACGATAACTTTTCACTT 4320  
Db 4261 TAAATGTTAAATTTGGTATTTCCAGAAATGATAAGCAATTTCTGTAACGATAACTTTTCACTT 4320  
QY 4321 GTGAATGCAATGATATGAGCATATGGAACAAACGGTCCACCAATGCGAAGTAAGCCGG 4380  
Db 4321 GTGAATGCAATGATATGAGCATATGGAACAAACGGTCCACCAATGCGAAGTAAGCCGG 4380  
QY 4381 TTATCACCAATATACGATTCATGACCAATTTCTAAGTTTGAAGTAACTATGACACTT 4440  
Db 4381 TTATCACCAATATACGATTCATGACCAATTTCTAAGTTTGAAGTAACTATGACACTT 4440  
QY 4441 TTTTGTTCGTAAACAGTCGGCAATAATATGAAATAGGAGCTCCGCTCTCTTCTTTTCAAAAT 4500  
Db 4441 TTTTGTTCGTAAACAGTCGGCAATAATATGAAATAGGAGCTCCGCTCTCTTCTTTTCAAAAT 4500  
QY 4501 GGTAATACCTAGTTCATCTAAAATTAATAATACAGGCTTCAATTTGCTTCTTTGATG 4560  
Db 4501 GGTAATACCTAGTTCATCTAAAATTAATAATACAGGCTTCAATTTGCTTCTTTGATG 4560  
QY 4561 CGGGTTAAATTCCTCTTTTAAAGCTCTTCTAATAGACCTACTAAATCTGCTACTCGG 4620  
Db 4561 CGGGTTAAATTCCTCTTTTAAAGCTCTTCTAATAGACCTACTAAATCTGCTACTCGG 4620  
QY 4621 AAAAACTTCACTTGTATATCCCTGTTCAACAGCTTCAAACTAATGCTGTAGCTAAATGT 4680  
Db 4621 AAAAACTTCACTTGTATATCCCTGTTCAACAGCTTCAAACTAATGCTGTAGCTAAATGT 4680  
QY 4681 GTTTTCCAGTCCAGAGATCCAGTAATAAGATTTTGTTCCTTCAAAAAATCGC 4740  
Db 4681 GTTTTCCAGTCCAGAGATCCAGTAATAAGATTTTGTTCCTTCAAAAAATCGC 4740  
QY 4741 AATTCAAAATGTCTTCTGATTCGTTGTAGATGGCAGATGAAATTTGTTTCACTTCAATTC 4800  
Db 4741 AATTCAAAATGTCTTCTGATTCGTTGTAGATGGCAGATGAAATTTGTTTCACTTCAATTC 4800  
QY 4801 TAAATCTTGAGCCATTTTAACTCTCGAAATTTTCGCTTTCTTGATTAAGTTTGTCTACTTTT 4860  
Db 4801 TAAATCTTGAGCCATTTTAACTCTCGAAATTTTCGCTTTCTTGATTAAGTTTGTCTACTTTT 4860  
QY 4861 TTCGTTTGACGAGATTCATCTCTATATGAAAAATATCAGCGAAATTTGTTCTTTGGTT 4920  
Db 4861 TTCGTTTGACGAGATTCATCTCTATATGAAAAATATCAGCGAAATTTGTTCTTTGGTT 4920  
QY 4921 TCAAAAGGATTTTCAATATGCTTATATATAGCTTAAATGCAAGTAAATTTACAGGCG 4980  
Db 4921 TCAAAAGGATTTTCAATATGCTTATATATAGCTTAAATGCAAGTAAATTTACAGGCG 4980

RESULT 2  
ADR89401  
ID ADR89401 standard; cDNA; 2082 BP.

QY 4981 TCTTCAGGTTTCGTTGTATCATATAGAAATGAAACCCCTTTCTAAAGTTGGACAAGCT 5040  
Db 4981 TCTTCAGGTTTCGTTGTATCATATAGAAATGAAACCCCTTTCTAAAGTTGGACAAGCT 5040  
QY 5041 TTTCGATCATATTCGTTGAAGATCTGTTTGGTAATCTATTTAAACACAGGTGGCGTATGGTTTT 5100  
Db 5041 TTTCGATCATATTCGTTGAAGATCTGTTTGGTAATCTATTTAAACACAGGTGGCGTATGGTTTT 5100  
QY 5101 CTTGGCAATTTTGTGATACGTCACCTGTTGAGTCTGCAATATGATATGATATGATATGATATGATATG 5160  
Db 5101 CTTGGCAATTTTGTGATACGTCACCTGTTGAGTCTGCAATATGATATGATATGATATGATATGATATG 5160  
QY 5161 GAGCTTTTTCACCAATCTCTTCAATCTCTTAAACAGTAAGTGTAGCTGCTGTAAATGAGTAT 5220  
Db 5161 GAGCTTTTTCACCAATCTCTTCAATCTCTTAAACAGTAAGTGTAGCTGCTGTAAATGAGTAT 5220  
QY 5221 TTTGAAATTAATATTTTGAATCTCTGTTTAAACAGCTTTTCTTTCATCTCTTATGAAAGAGCA 5280  
Db 5221 TTTGAAATTAATATTTTGAATCTCTGTTTAAACAGCTTTTCTTTCATCTCTTATGAAAGAGCA 5280  
QY 5281 GATAATCTTGAACCCGCTGAGGTAAATATTTGAAAAATCTAGAAATAACGAAACAAACGCGTG 5340  
Db 5281 GATAATCTTGAACCCGCTGAGGTAAATATTTGAAAAATCTAGAAATAACGAAACAAACGCGTG 5340  
QY 5341 GTTTCCTTTTCCCAATCTCTTCCCATAGAAATCGGCCCTTACTCGTGTGCAATAT 5400  
Db 5341 GTTTCCTTTTCCCAATCTCTTCCCATAGAAATCGGCCCTTACTCGTGTGCAATAT 5400  
QY 5401 ACGGTCTGTATTTCTGTAAATAATGTTCTCGCCTTCTGCGGTATAACATGTAATATGATCC 5460  
Db 5401 ACGGTCTGTATTTCTGTAAATAATGTTCTCGCCTTCTGCGGTATAACATGTAATATGATCC 5460  
QY 5461 ATTCTTTTAAATGATATCACTCTGTTTACGTAAAAACAAAAACGTTCTTGTATCCACTGTG 5520  
Db 5461 ATTCTTTTAAATGATATCACTCTGTTTACGTAAAAACAAAAACGTTCTTGTATCCACTGTG 5520  
QY 5521 ATTCTCCATATTTATTTACCGTTGTGTCCATGTAGAAAGACCGTTAGGTCTTCCAAA 5580  
Db 5521 ATTCTCCATATTTATTTACCGTTGTGTCCATGTAGAAAGACCGTTAGGTCTTCCAAA 5580  
QY 5581 GGTAATGGTTTCAATGCAGCCTTATCATCATTTCCAAAGGTCTTCAATCATGACTTCCCTTC 5640  
Db 5581 GGTAATGGTTTCAATGCAGCCTTATCATCATTTCCAAAGGTCTTCAATCATGACTTCCCTTC 5640  
QY 5641 TCAATATGTAGCGGTTCTGATCTTCTATTTGCTGTACTTCTAAACCATTTGCGAGTTGA 5700  
Db 5641 TCAATATGTAGCGGTTCTGATCTTCTATTTGCTGTACTTCTTCTAAACCATTTGCGAGTTGA 5700  
QY 5701 GAAAACTCTCCATATCGGAGCGGTTGTAACCAATTTGTTTGGTGTATACTGACTTTC 5760  
Db 5701 GAAAACTCTCCATATCGGAGCGGTTGTAACCAATTTGTTTGGTGTATACTGACTTTC 5760  
QY 5761 CGTTCAACGTTCCCTTTTTCATGCCGCTATGAGGTTTCAAGGTTGCAAGTTTCAAAAGTTA 5820  
Db 5761 CGTTCAACGTTCCCTTTTTCATGCCGCTATGAGGTTTCAAGGTTGCAAGTTTCAAAAGTTA 5820  
QY 5821 TAAATGATTTGAAATTTGAAAAATGATCCGTTAAGTTTCGATTAATCATCTTTTCTTACT 5880  
Db 5821 TAAATGATTTGAAATTTGAAAAATGATCCGTTAAGTTTCGATTAATCATCTTTTCTTACT 5880  
QY 5881 GTGACTACAGCGCAGATTAAGTTTCAATTCGAAAGATGCGTTGGTACACACAGCTTGA 5940  
Db 5881 GTGACTACAGCGCAGATTAAGTTTCAATTCGAAAGATGCGTTGGTACACACAGCTTGA 5940  
QY 5941 TGAATAATTCGTTTAAAGCCTTCTAAAAAGCCTTCTGTAT 5980  
Db 5941 TGAATAATTCGTTTAAAGCCTTCTAAAAAGCCTTCTGTAT 5980

XX AC ADR89401;  
 XX XX 18-NOV-2004 (first entry)  
 XX DE AXMI-008 coding sequence.  
 XX KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
 KW expression cassette; transformation; transgenic; plant; bacteria;  
 KW lepidoptera; coleoptera; pest; pesticide; resistance;  
 KW pesticidal activity.  
 XX OS Bacillus thuringiensis.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..2082  
 FT /\*tag= a  
 FT /product= "AXMI-008"  
 FT /transl\_except= pos:1..3, aa:Met  
 XX WO2004074462-A2.  
 XX PN 02-SEP-2004.  
 XX PD 20-FEB-2004; 2004WO-US005829.  
 XX PF 20-FEB-2003; 2003US-0448632P.  
 XX PR 20-FEB-2003; 2003US-0448633P.  
 XX PR 20-FEB-2003; 2003US-0448797P.  
 XX PR 20-FEB-2003; 2003US-0448806P.  
 XX PR 20-FEB-2003; 2003US-0448810P.  
 XX PR 20-FEB-2003; 2003US-0448812P.  
 XX PR 19-FEB-2004; 2004US-00781979.  
 XX PR 19-FEB-2004; 2004US-00782020.  
 XX PR 19-FEB-2004; 2004US-00782096.  
 XX PR 19-FEB-2004; 2004US-00782141.  
 XX PR 19-FEB-2004; 2004US-00782570.  
 XX PR 19-FEB-2004; 2004US-00783417.  
 XX PA (ATHE-) ATHENIX CORP.  
 XX PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 XX DR WPI; 2004-635574/61.  
 XX DR P-PSDB; ADR89402.  
 XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 XX PS Claim 1; SEQ ID NO 13; 178pp; English.  
 XX CC This sequence encodes an isolated delta-endotoxin. Some of the delta-  
 CC endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.  
 XX SQ Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;  
 Query Match 34.8%; Score 2082; DB 13; Length 2082;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GTGAAAGATGAGTCCATATCAAAATGAAATATGAAATATGGAATCTCATCG 227  
 DB 1 GTGAAAAGATGAGTCCATATCAAAATGAAATATGAAATATGGAATCTCATCG 60  
 QY 228 AATAACACAATAAGCCAAACAGATATCCTTTTGCAAAATATCGGATATGTCTACTATG 287  
 DB 61 AATAACACAATAAGCCAAACAGATATCCTTTTGCAAAATATCGGATATGTCTACTATG 120  
 QY 288 TCTTGGAAATGATTGTGAGGGAATCTCATGGATGAAATTTGGAAATCAGTCGAAACGATA 347  
 DB 121 TCTTGGAAATGATTGTGAGGGAATCTCATGGATGAAATTTGGAAATCAGTCGAAACGATA 180  
 QY 348 ACAAGTATGGGATAAATCTTATAGAGTTTGTATAGAACCTAGTTTGGGTGGAATTAAT 407  
 DB 181 ACAAGTATGGGATAAATCTTATAGAGTTTGTATAGAACCTAGTTTGGGTGGAATTAAT 240  
 QY 408 ACATATATCAATAATAGGAAACCTAATTTCCGACTAATCGTCAAACTGTGTGAGCACTT 467  
 DB 241 ACATATATCAATAATAGGAAACCTAATTTCCGACTAATCGTCAAACTGTGTGAGCACTT 300  
 QY 468 TCTATATGTGATTTATTTATCTATATCGTAAAGAGGTAGCCGATAGTGTGTAAGTGAT 527  
 DB 301 TCTATATGTGATTTATTTATCTATATCGTAAAGAGGTAGCCGATAGTGTGTAAGTGAT 360  
 QY 528 GCGATTGCAGATTTTGACCGTAAATTTGAAAAATTTATAGAGAGTATTATCTTCTTATCTT 587  
 DB 361 GCGATTGCAGATTTTGACCGTAAATTTGAAAAATTTATAGAGAGTATTATCTTCTTATCTT 420  
 QY 588 GGGCTTGGCTTAAAGACCGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAA 647  
 DB 421 GGGCTTGGCTTAAAGACCGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAA 480  
 QY 648 TTAGTTTATTTTAAACCTTTTCAAGAGAGATTTCAATGAAATTTCTAGAGAGGTCTATTG 707  
 DB 481 TTAGTTTATTTTAAACCTTTTCAAGAGAGATTTCAATGAAATTTCTAGAGAGGTCTATTG 540  
 QY 708 TCAAGAAACAATGCTCAAGTATTGTTTATACCTACTTTTGCACAAGCTGCAAAATGTGCGAG 767  
 DB 541 TCAAGAAACAATGCTCAAGTATTGTTTATACCTACTTTTGCACAAGCTGCAAAATGTGCGAG 600  
 QY 768 TTATTTACTATTAGGGATGAGTTCAATATAAAGCACAATGGTTCCATTTTTGAGTGCA 827  
 DB 601 TTATTTACTATTAGGGATGAGTTCAATATAAAGCACAATGGTTCCATTTTTGAGTGCA 660  
 QY 828 GAGAATGTAAGATCGGAATTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTAC 887  
 DB 661 GAGAATGTAAGATCGGAATTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTAC 720  
 QY 888 TATGAGCGATTAAATGCAAAACGGCAGAGATATACCAATTTATGTTTATATTCGTTATCAG 947  
 DB 721 TATGAGCGATTAAATGCAAAACGGCAGAGATATACCAATTTATGTTTATATTCGTTATCAG 780  
 QY 948 GTAGGTTTAAATCAGATAAACAAGGGGGGAGCAGGTGCTGACACTTTGGTCGAAATTAAT 1007  
 DB 781 GTAGGTTTAAATCAGATAAACAAGGGGGGAGCAGGTGCTGACACTTTGGTCGAAATTAAT 840  
 QY 1008 AAATTTCTGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCACACTTAT 1067  
 DB 841 AAATTTCTGAGAAATGACGTTGGCGGTATTGGATATTATTCGCTATATTTCACACTTAT 900  
 QY 1068 GATTTTGGAAATATCCATTTGCCAACACATGTAGAGTTCAGTAGGGAATTTTATACAGAT 1127  
 DB 901 GATTTTGGAAATATCCATTTGCCAACACATGTAGAGTTCAGTAGGGAATTTTATACAGAT 960  
 QY 1128 GCAGTGGGATATTCATTCGGGAACTTATAGTTGGTTACCGGAATTTGGCCTAATTAAT 1187  
 DB 961 GCAGTGGGATATTCATTCGGGAACTTATAGTTGGTTACCGGAATTTGGCCTAATTAAT 1020  
 QY 1188 GGGTTAGAGCGTAATGGAAACACGGGACCTGGTTTGTAGTTACTTTGGCTTACGAAAAATAGGT 1247  
 DB 1021 GGGTTAGAGCGTAATGGAAACACGGGACCTGGTTTGTAGTTACTTTGGCTTACGAAAAATAGGT 1080  
 QY 1248 ATATATAATGAGTATGTTTTCGAGATATTTTTCGGCGGTGGTAGGAACCTCGTCATTATGAA 1307

Db 1081 ATATATAATAGATGTTTCGAGATATTTTGC CGCTGGGTAGGAATCTCGTCATTATGAA 1140  
QY GACTACAAAGGGTAACGGTATTTTTCAACGATGTCCTGGAACTACGAGTAGTATGATCTA 1367  
Db 1141 GACTACAAAGGGTAACGGTATTTTTCAACGATGTCCTGGAACTACGAGTAGTATGATCTA 1200  
QY CGTAATATTGATTTTCAGAAATGCCGATGTATATAAATAATCTTTCATTAGCTATCATGAAC 1427  
Db 1201 CGTAATATTGATTTTCAGAAATGCCGATGTATATAAATAATCTTTCATTAGCTATCATGAAC 1260  
QY CTAGTAGGAGAGACTACCGCTAGACCGAGATATCGTGTTCAAAGCAGATTTTCCTAGG 1487  
Db 1261 CTAGTAGGAGAGACTACCGCTAGACCGAGATATCGTGTTCAAAGCAGATTTTCCTAGG 1320  
QY GTAGGGGACCTGATTTAAATATGATGACGAGTAAATGCGGCTAAGCAGGATGACAAAT 1547  
Db 1321 GTAGGGGACCTGATTTAAATATGATGACGAGTAAATGCGGCTAAGCAGGATGACAAAT 1380  
QY GAATCTACGTTCCCACTTGTTATGCACTCTAATGCTGTAGAGACCCCTCTCATAGATTA 1607  
Db 1381 GAATCTACGTTCCCACTTGTTATGCACTCTAATGCTGTAGAGACCCCTCTCATAGATTA 1440  
QY TCAATGCGGCATGCTGTATATGCAAACTCCAGAGTTAAACGTATATGCTTGGACACAT 1667  
Db 1441 TCAATGCGGCATGCTGTATATGCAAACTCCAGAGTTAAACGTATATGCTTGGACACAT 1500  
QY ACAAGTTTAAACGTTGAAATATAATGAAAGCAATCAAAATACCAAAATACCGCGGGTG 1727  
Db 1501 ACAAGTTTAAACGTTGAAATATAATGAAAGCAATCAAAATACCAAAATACCGCGGGTG 1560  
QY AGAGTTATTACCTTCAAAATATTCTGTGTAATGCTTACCTATACCTATGTAATAAAGCACT 1787  
Db 1561 AGAGTTATTACCTTCAAAATATTCTGTGTAATGCTTACCTATACCTATGTAATAAAGCACT 1620  
QY CATACAGTGGGATTTAATCCGTTTAAAGCAAAATACAGAGTATACCGAGTTTAT 1847  
Db 1621 CATACAGTGGGATTTAATCCGTTTAAAGCAAAATACAGAGTATACCGAGTTTAT 1680  
QY GCAGGTGGCGGAATTAGATTGATTATTAATAACAAATCGCAGGACAAAGTTACCGTAT 1907  
Db 1681 GCAGGTGGCGGAATTAGATTGATTATTAATAACAAATCGCAGGACAAAGTTACCGTAT 1740  
QY CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1967  
Db 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800  
QY TGGGGTTCAAATCGTTTGTATCGCTTGAAATCTTACTCTGGAATATGACGATTTA 2027  
Db 1801 TGGGGTTCAAATCGTTTGTATCGCTTGAAATCTTACTCTGGAATATGACGATTTA 1860  
QY AAATATAGTATGATTTTAAATTCGCTGAAATATCACACCTCCATTTACCTAGTTCAAAAT 2087  
Db 1861 AAATATAGTATGATTTTAAATTCGCTGAAATATCACACCTCCATTTACCTAGTTCAAAAT 1920  
QY CAGATGGATGTGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACCGTGTCTCGAC 2147  
Db 1921 CAGATGGATGTGAGATGCAAGCGAATAGTTTTCAATCAGATGTAACCGTGTCTCGAC 1980  
QY AAAATTTGAATTCCTCCCAAGTATACAACTTTAGATATGAGGAGAACGGGACCTA 2207  
Db 1981 AAAATTTGAATTCCTCCCAAGTATACAACTTTAGATATGAGGAGAACGGGACCTA 2040  
QY GAAAAACAAAGAACCGGTGACGATCTGTTTACCAATTA 2249  
Db 2041 GAAAAACAAAGAACCGGTGACGATCTGTTTACCAATTA 2082

RESULT 3  
ID ADR89403  
AC ADR89403 standard; cDNA; 2073 BP.

XX DT 18-NOV-2004 (first entry)  
XX AXMI-008 alternative start site coding sequence.  
XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
XX pesticidal activity.  
OS Bacillus thuringiensis.  
XX Key Location/Qualifiers  
FH 1. .2073  
FT CDS /\*tag= a  
FT /product= "Alternative AXMI-008"  
XX PN WO2004074462-A2.  
XX PD 02-SEP-2004.  
XX PF 20-FEB-2004; 2004WO-US005829.  
XX PR 20-FEB-2003; 2003US-0448632P.  
PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.  
PR 20-FEB-2003; 2003US-0448806P.  
PR 20-FEB-2003; 2003US-0448810P.  
PR 20-FEB-2003; 2003US-0448812P.  
PR 19-FEB-2004; 2004US-00781979.  
PR 19-FEB-2004; 2004US-00782020.  
PR 19-FEB-2004; 2004US-00782096.  
PR 19-FEB-2004; 2004US-00782141.  
PR 19-FEB-2004; 2004US-00782570.  
PR 19-FEB-2004; 2004US-00783417.  
XX (ATHE-) ATHENIX CORP.  
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
WPI: 2004-635574/61.  
P-PSDB; ADR89404.  
XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.  
XX Claim 1; SEQ ID NO 15; 178pp; English.  
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.  
XX Sequence 2073 BP; 694 A; 305 C; 431 G; 643 T; 0 U; 0 Other;  
SQ Query Match 34.7%; Score 2073; DB 13; Length 2073;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 ATGAGTCCATATCAAAATAAAAAATGAATATGAATATTCGAAATCCTCATCGAATAACACA 236  
Db 1 ATGAGTCCATATCAAAATAAAAAATGAATATGAATATTCGAAATCCTCATCGAATAACACA 60

QY 237 AATACGCCAACACAGATATCTTTTGCAGAAATTAATCGGATATGTCTACTATGTCTTTGGAAT 296  
DB 61 AATACGCCAACACAGATATCTTTTGCAGAAATTAATCGGATATGTCTACTATGTCTTTGGAAT 120  
QY 297 GATTGTGAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 356  
DB 121 GATTGTGAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT 180  
QY 357 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAACACTATTA 416  
DB 181 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAACACTATTA 240  
QY 417 TCRAATAATAGGAAACTAAATCCGACTAAATCGTCAAACTGTGTGAGCACTTTTCTATATGT 476  
DB 241 TCRAATAATAGGAAACTAAATCCGACTAAATCGTCAAACTGTGTGAGCACTTTTCTATATGT 300  
QY 477 GATTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTAACTGATGCGATTGCA 536  
DB 301 GATTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTAACTGATGCGATTGCA 360  
QY 537 GATTTTCACGCTAAATTTGAAATAATTAGAGAGTATTATCTTTCTTATCTTTGGGCTTG 596  
DB 361 GATTTTCACGCTAAATTTGAAATAATTAGAGAGTATTATCTTTCTTATCTTTGGGCTTG 420  
QY 597 CTTAAAGACGCTAAACCACTTTCAAAAGACAAATAATCTGATATCGGACAAATAGTTTAT 656  
DB 421 CTTAAAGACGCTAAACCACTTTCAAAAGACAAATAATCTGATATCGGACAAATAGTTTAT 480  
QY 657 TATTTTAACTTTTCAGAAAGAGATTTCAATGAAATCTAGGAGGTCAATTTGTCAGAAAC 716  
DB 481 TATTTTAACTTTTCAGAAAGAGATTTCAATGAAATCTAGGAGGTCAATTTGTCAGAAAC 540  
QY 717 AATGCTCAAGTATGTATTACCTACTTTTGCACAACTGCAATGTGCAAGTATTACTA 776  
DB 541 AATGCTCAAGTATGTATTACCTACTTTTGCACAACTGCAATGTGCAAGTATTACTA 600  
QY 777 TTAAGGATGCAGTTCATATAAAGCAACAATGGTTCCTCATTTTGTAGTCAGAGAAATGTA 836  
DB 601 TTAAGGATGCAGTTCATATAAAGCAACAATGGTTCCTCATTTTGTAGTCAGAGAAATGTA 660  
QY 837 AGATCGGAATTAATATACCTAAACAGTGGTGTGATTTTACCGGTGATTAATGAGCGA 896  
DB 661 AGATCGGAATTAATATACCTAAACAGTGGTGTGATTTTACCGGTGATTAATGAGCGA 720  
QY 897 TTAATAATGCAAAACGCGAGATATACCAATATTTGTTATTTGTTATGTTATGAGTATTG 956  
DB 721 TTAATAATGCAAAACGCGAGATATACCAATATTTGTTATTTGTTATTTGTTATGAGTATTG 780  
QY 957 AATCAGATAAACAAGGGGGGACAGGTGCTGACACTTTGGTCGAAATTTTAAATAATTTTCGT 1016  
DB 781 AATCAGATAAACAAGGGGGGACAGGTGCTGACACTTTGGTCGAAATTTTAAATAATTTTCGT 840  
QY 1017 AGAGAAATGAGTGGCGGTATTGGATTTATTCGCTATATTTTCCAACTTATGATTTGAG 1076  
DB 841 AGAGAAATGAGTGGCGGTATTGGATTTATTCGCTATATTTTCCAACTTATGATTTGAG 900  
QY 1077 AATATCCATTTGCCAACACATGTAGAGTTGACCTAGGGAATTTATACAGATGAGTGGGA 1136  
DB 901 AATATCCATTTGCCAACACATGTAGAGTTGACCTAGGGAATTTATACAGATGAGTGGGA 960  
QY 1137 TATTTCATCGGGAATCTTATAGTTGGTTACGGAAATTTGGCTAATCTTTTAAATGGTTAGAG 1196  
DB 961 TATTTCATCGGGAATCTTATAGTTGGTTACGGAAATTTGGCTAATCTTTTAAATGGTTAGAG 1020  
QY 1197 GCTAATGGAAACAAGGGGACTGTTTGTAGTTTACTGCTTAGCAAAATAGGTATATATAAT 1256  
DB 1021 GCTAATGGAAACAAGGGGACTGTTTGTAGTTTACTGCTTAGCAAAATAGGTATATATAAT 1080  
QY 1257 GAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTGCTATTATGAAGACTACACA 1316  
DB 1081 GAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTGCTATTATGAAGACTACACA 1140

QY 1317 AAGGTAACCGGTATTTTTCACGATGTCTCTGGAACTACGAGTAATGATCTACGTAATATT 1376  
DB 1141 AAGGTAACCGGTATTTTTCACGATGTCTCTGGAACTACGAGTAATGATCTACGTAATATT 1200  
QY 1377 GATTTTCAGAAATCCGATGTATATAAAATTTACTTTCAATAGCTATCATGAACCTAGTAGGA 1436  
DB 1201 GATTTTCAGAAATCCGATGTATATAAAATTTACTTTCAATAGCTATCATGAACCTAGTAGGA 1260  
QY 1437 GAGACTACCGCTAGACGAGATATCGTGTTCCTCAAGGCAGATTTTCGTAAGGTAGGGGGA 1496  
DB 1261 GAGACTACCGCTAGACGAGATATCGTGTTCCTCAAGGCAGATTTTCGTAAGGTAGGGGGA 1320  
QY 1497 CCTGATTTAAATTTATGATGAGGTAAATTAATGGGCTAAGCAGGATGACAAATTTGAATCTACG 1556  
DB 1321 CCTGATTTAAATTTATGATGAGGTAAATTAATGGGCTAAGCAGGATGACAAATTTGAATCTACG 1380  
QY 1557 TTCCCACTTTGTATTTGCACTCTAAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCG 1616  
DB 1381 TTCCCACTTTGTATTTGCACTCTAAATGGTGTAGAGGACCTCTCATAGATTTATCAAAATGCG 1440  
QY 1617 GCATGTGTGTATATGGAACTCCAGAGTTAAACGTATATGGTTGGACACATACAAAGTTTA 1676  
DB 1441 GCATGTGTGTATATGGAACTCCAGAGTTAAACGTATATGGTTGGACACATACAAAGTTTA 1500  
QY 1677 AAACGTGAAATATAATTTGAAGCAATCAAAATTTACAAATACCGGCGGTGAAGAGTTAT 1736  
DB 1501 AAACGTGAAATATAATTTGAAGCAATCAAAATTTACAAATACCGGCGGTGAAGAGTTAT 1560  
QY 1737 TACCTTTCAAAATTTATCTTGTAAATGGCTATACCTATGTATTAATAAAGGCACCTACACAGGT 1796  
DB 1561 TACCTTTCAAAATTTATCTTGTAAATGGCTATACCTATGTATTAATAAAGGCACCTACACAGGT 1620  
QY 1797 GGGGATTTAACTCGTGTTCCTTTTAAAGAACAAATACAGAGTATTAACGAGTTTATGACAGGTGGC 1856  
DB 1621 GGGGATTTAACTCGTGTTCCTTTTAAAGAACAAATACAGAGTATTAACGAGTTTATGACAGGTGGC 1680  
QY 1857 GGAATTTAGATTGATTAATTAATAACAAATCTGACAGGACAAAGTTTACCGTATTTTCGT 1916  
DB 1681 GGAATTTAGATTGATTAATTAATAACAAATCTGACAGGACAAAGTTTACCGTATTTTCGT 1740  
QY 1917 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTTATCCAGAGGTTGGGGTTCA 1976  
DB 1741 TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTTATCCAGAGGTTGGGGTTCA 1800  
QY 1977 AATCGTTTTGTATCGCTTGAATAATCTTACTCTGGAATAATGACGATTTAAATATAGT 2036  
DB 1801 AATCGTTTTGTATCGCTTGAATAATCTTACTCTGGAATAATGACGATTTAAATATAGT 1860  
QY 2037 GATTTTAAATTCGCTCAAAATTTATCACACCTCCATTTACCTTCCAAATTTCAAGATCGAT 2096  
DB 1861 GATTTTAAATTCGCTCAAAATTTATCACACCTCCATTTACCTTCCAAATTTCAAGATCGAT 1920  
QY 2097 GTGAGATCAAGCGGAATAGTTTTCATCAGATGTAAACGTGGTTCTTCGACAAAATTTGAA 2156  
DB 1921 GTGAGATCAAGCGGAATAGTTTTCATCAGATGTAAACGTGGTTCTTCGACAAAATTTGAA 1980  
QY 2157 TTCTCTCCAAAGTAATACAACTTTAGAAATAGAGGAGAACCGGACCTAGAAAAACA 2216  
DB 1981 TTCTCTCCAAAGTAATACAACTTTAGAAATAGAGGAGAACCGGACCTAGAAAAACA 2040  
QY 2217 AAGAACCGGCTGAACGATCTGTTTACCAATTTAA 2249  
DB 2041 AAGAACCGGCTGAACGATCTGTTTACCAATTTAA 2073

RESULT 4

ADR89405

ID ADR89405 standard; cDNA; 1686 BP.

XX ADR89405;

AC ADR89405;

XX 18-NOV-2004 (first entry)

DT





Db 1141 CAACAAATGGATGGAGCTTCAGTATTAGTCTCTCAAAATGGAGCGGGGTATCTCAA 1200  
 Qy 3509 AACTTGCAATGCTCAAGATCATCATGATATGTTAGTGTGATTCGCAAAAGAGGA 3568  
 Db 1201 AACTTGCAATGCTCAAGATCATCATGATATGTTAGTGTGATTCGCAAAAGAGGA 1260  
 Qy 3569 CCTGGAAGGGTATGTAACGATGATGGATTGTAATGGAAGCAGGAAACACATTAAGTTC 3628  
 Db 1261 CCTGGAAGGGTATGTAACGATGATGGATTGTAATGGAAGCAGGAAACACATTAAGTTC 1320  
 Qy 3629 ACTTCTTCCGGAAGGATATATACAAAGACAGTAGAGGTATTCGCAAAAGTATCGT 3688  
 Db 1321 ACTTCTTCCGGAAGGATATATACAAAGACAGTAGAGGTATTCGCAAAAGTATCGT 1380  
 Qy 3689 GTACGGATTGAATAGGAGAAACGAAAGGTACATTTATATAGATAGCATCGAGTTCCTT 3748  
 Db 1381 GTACGGATTGAATAGGAGAAACGAAAGGTACATTTATATAGATAGCATCGAGTTCCTT 1440  
 Qy 3749 TGTATGCAAGGATATGATAAATTAATTAACCTGCACACGGGTATATGATGAGCAAAAGT 3808  
 Db 1441 TGTATGCAAGGATATGATAAATTAATTAACCTGCACACGGGTATATGATGAGCAAAAGT 1500  
 Qy 3809 TATTAATGGAATTAATTAATCAAAATCTAGCGATGTGTATTAACCAAGGGTATACAAACAC 3868  
 Db 1501 TATTAATGGAATTAATTAATCAAAATCTAGCGATGTGTATTAACCAAGGGTATACAAACAC 1560  
 Qy 3869 TATAACCAAGACTCTAGTATATGTAATTAATCAAAATCTAGCGATGTGTATTAACCAAGGGTATAC 3928  
 Db 1561 TATAACCAAGACTCTAGTATATGTAATTAATCAAAATCTAGCGATGTGTATTAACCAAGGGTATAC 1620  
 Qy 3929 TCCGGTTGCACATGTAACCAAGGGCAATACTCTGGCTGTACATGTAATCAAGGATATAAC 3988  
 Db 1621 TCCGGTTGCACATGTAACCAAGGGCAATACTCTGGCTGTACATGTAATCAAGGATATAAC 1680  
 Qy 3989 CGTTAA 3994  
 Db 1681 CGTTAA 1686

RESULT 5  
 AEA61394  
 ID AEA61394 standard; DNA; 4391 BP.  
 AC AEA61394;  
 XX  
 DT 11-AUG-2005 (first entry)  
 XX  
 DE Bacillus thuringiensis Cry19Aa coding sequence, SEQ ID 4.  
 XX  
 KW Insecticide; crystal protein; Cry19Aa; gene; da.  
 XX  
 OS Bacillus thuringiensis.  
 XX  
 FH Key Location/Qualifiers  
 CDS 719..2665  
 FT /\*tag= a  
 FT /product= "Cry19Aa"  
 XX  
 PN US2005124803-A1.  
 XX  
 PD 09-JUN-2005.  
 XX  
 PF 30-AUG-2004; 2004US-00929754.  
 XX  
 PR 29-AUG-2003; 2003US-0498826P.  
 XX  
 PA (OHIS ) UNIV OHIO STATE RES FOUND.  
 XX  
 PI Dean DH, Abdullah MA;  
 XX  
 DR WPI; 2005-417057/42.  
 DR P-PSDB; AEA61393.  
 DR EMBL; Y07603.

XX

PT New modified *Bacillus thuringiensis* insecticidal crystal proteins (i.e. Cry4Ba and Cry19Aa) with enhanced toxicity, useful for reducing or eliminating populations of target insects (i.e. mosquitoes) that are vectors of disease.

PS Disclosure; SEQ ID NO 4; 63pp; English.

CC The present invention relates to modified insecticidal *Bacillus thuringiensis* crystal proteins Cry4Ba and Cry19Aa which have enhanced toxicity against a variety of insects, e.g. mosquitoes and lepidoptera. The modified proteins are useful for reducing or eliminating populations of target insects that are vectors of disease, particularly mosquitoes. CC The present sequence is the coding sequence of the wild-type Cry19Aa protein, which can be modified with: a substitution of amino acids at positions 355 through 358 with amino acids tyrosine, glutamine, aspartic acid, and leucine; an insertion of at least one amino acid (e.g. arginine) after position 358 and a deletion of the amino acids at positions 414 through 418.

SQ Sequence 4391 BP; 1557 A; 630 C; 914 G; 1290 T; 0 U; 0 Other;

Query Match 16.2%; Score 967; DB 14; Length 4391;  
 Best Local Similarity 74.8%; Pred. No. 2.1e-166;  
 Matches 1296; Conservative 0; Mismatches 409; Indels 27; Gaps 6;

Qy 2143 TCACAAAAATTGAATTCCTCCCAAGTA----ATACAACTTTAGAAATATGAGGAGAA 2198  
 Db 2634 TAGATAAAATCGAATTCCTCCCAACTGATACCAATTCACAGGAATATGAGGAATA 2693  
 Qy 2199 CGGGACCTAGAAAAACAAGAACGGGTGAACGATCTGTTTACCATTATTAACAAAAATA 2258  
 Db 2694 TATGAATTAAGAAAGATCAGAGGAACATTTAATAGTATATTTGTTGATTAACAAAAAG-- 2751  
 Qy 2259 ATTTACTAGAAATAGTGGTATTGCTGTTTAAACAAATAAGCGAAAAAGGTTGTGAGTCCTA 2318  
 Db 2752 ---TACTAACGTAGATGGTATAGCTGTTTGAAAAATAAGAAAAAGGTTGTGAATTTTA 2808  
 Qy 2319 TGTTTACAAGTAGTAGCAAAAAATACGTTAAAAATAGAACGACAGATATTGAATATAGATC 2378  
 Db 2809 TGCTTACAAGTGTGTGCGAAAAATATGTTAAAACTCGAAACGACAGATATTGAATATAGATC 2868  
 Qy 2379 AAGCGGCCATTTCTATAGAAATGATGTCAGATGAACAAATCTCTCAGGAAAAAATATGT 2438  
 Db 2869 AATGGCGAATGCTATAGAAATATGTCAGGTGAACAATATTCACAGGAAAAAATATGATC 2928  
 Qy 2439 TATGGGATGAATATAAACTGGCAAAAACAACTTAGTCACTCTCGTAATCTACTCCAAAATG 2498  
 Db 2929 AATGGCATGACATAAAATATGCCAAACAATTGAGTCAAGCACGTAATTTACTTCAAAATG 2988  
 Qy 2499 GAGACTT-----TTCGGGAATGATGGACATTCGGTAAATGATATATCATAGGATCCA 2552  
 Db 2989 GTGAATTTGAGGATTTATTTAGTGGATGGACTACAAGTAAATCAGATGTCCATTCAGGCAG 3048  
 Qy 2553 ATAATCCTATTTTAAAGGAAAAATTTCTACAGATGCGTGGAGCAGCAGACATATATGGAA 2612  
 Db 3049 ATANTGCAACTTTTAAAGGAACTATCTGCATATGCTGGGGGAGAGACATATATGGAA 3108  
 Qy 2613 CTCTATTTCCAACTTATCTGTCAAAAAATAGATGAGTCTTAAATTTAAAAACCAATATACAC 2672  
 Db 3109 CGATATTTCCCAAGTATATATACCAAAAAATTTGATGAATCCAAATTTAAACCGTATACGC 3168  
 Qy 2673 GTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAGATTTGAAATTTAATGGTAACAGTTT 2732  
 Db 3169 GTTATCTAGTCAGGGGATTTGTGGGAAGTAGTAAGATCTAGAAATTTAATGGTAATGCGTT 3228  
 Qy 2733 ACGGGAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATACACGCTTA 2792  
 Db 3229 ATGGAAGAAATTTGATACAGTAATGAATGTACCAATGACATACCGTACGTACCTTCTA 3288  
 Qy 2793 ATCCTTTTCATGT---GGAGATTATTCGCTGTGAATCATCGTCTCAGTATGTGAGCAAGGGT 2849  
 Db 3289 TGCCTGCTGTAACGAATTTATGATGGTCAACAACCGTATCCAAATAGGCATGTAGGAT 3348



|    |      |  |      |
|----|------|--|------|
| Qy | 49   | AAATAATGGGGTTATTTGTAGAAACATTTGTTACAGGAATACATTTGGGGTACTACGAATAT   | 108  |
| Db | 8    | AAATAATATGTTTTTTGTAGAAACATTTGTTACAGGAATACATTTGGGGTACTACGAATAT    | 67   |
| Qy | 109  | ATAGAAAGACACCTAAACATATATTTATPAGTGTCTTAAATAATPAGACTATATAAGGAG     | 168  |
| Db | 68   | ATAGAAAGACACCTGGCANATATTTATPAGTGTCTTAAATAATPAGACTATATAAGGAG      | 127  |
| Qy | 169  | TGAAAAAGATGAGTCCATATCAAAATAAAAAATGAAATATGAAATATTTGGAAATCCATCGA   | 228  |
| Db | 128  | TGAAAAATATGAAATTCCTTACAAAATACAAATGAATATGAAATCTCGATGGTTCGCCGA     | 187  |
| Qy | 229  | ATAACACAAATACGCCAAAACAGATATCCTTTTGGCAATAATATCGGGATATGTCTACTATGT  | 288  |
| Db | 188  | ATAACACAAATATGTCAACACAGATATCCTTTTGCAAAGGATCCAAAATATATTTCTCTATTA  | 247  |
| Qy | 289  | CTTCGAATGATGTGACGGAACTCATCGGAATGAAATTTGGGAATCAGTCGGAATATAG       | 348  |
| Db | 248  | ACCTGGACGTTGTTCAGGAAGGCCATGGCAAGATACGTGGGAATCAGTCCTCGGATATAG     | 307  |
| Qy | 349  | CAAGTATTTGGGATAAAATCTTATAGAGTTTGTGTAGAACCTPAGTTTGGGTGGAATTAATA   | 408  |
| Db | 308  | TAACTATTTGGGACATCCTTATACAATCTTGTCTAGAACCCGGTATAGTGGAAATTCCTG     | 367  |
| Qy | 409  | CACATATATCAATAATAGGAAAACTAATTCGCACTAATCGTCAAACTGTGTGACACATTT     | 468  |
| Db | 368  | TAATATTTTCAATAATAAAACAACTCAATCCGTCTCTGTGTCAACTGTGTGACACATTT      | 427  |
| Qy | 469  | CTATATCTGATTTATATCTATATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAGTATG     | 528  |
| Db | 428  | CTATATGTGATTTAGTATCTATAATTCGTAAAGAGGTAGACGAGCGGTGTAAGTGACG       | 487  |
| Qy | 529  | CGATTGCAGATTTTGACCGTAAATTTGAAAAATTTATAGAGATATTTCTTCTTTTATCTTG    | 588  |
| Db | 488  | GGGTTCAGATTTTGAGGTCGAATGACTGCTTATCAAGTATATATCTTCATTTATCTTG       | 547  |
| Qy | 589  | GGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAAATAATCTTGATATCGCAAT      | 648  |
| Db | 548  | AGGATTTGGCTTACAG-----ATAAATCAAACTCTTAAAAAACTTCTGTGACG            | 592  |
| Qy | 649  | TAGTTTATTTTAAACTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCATTTG       | 708  |
| Db | 593  | TAGTTTAAACAGTTCCAAAGCAGCGGAAGAAGATTTCTACTAACTTTTACGAGGGTCATTT    | 652  |
| Qy | 709  | CAAGAAAACAATGCTCAAGTATTTGTTATTAATCCTACTTTTGCAACAGCTGCAAAATGTCAGT | 768  |
| Db | 653  | CAAGACAGAAGCTGAATATATTTATGCTACGTATGTGCAAGCTGCAAAATGTCGATTT       | 712  |
| Qy | 769  | TATTACTATTAAAGGATGCAAGTTCOAATATAAAGCACAAATGGTTCCTTATTTTGAGTGCAG  | 828  |
| Db | 713  | TATTACTATTAAAGGACCGAGTTAAATATAAAAAAGAAATGGGACTAGTGTGTCCACCGT     | 772  |
| Qy | 829  | AGATGTAAAGTCGGAATTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTTACT      | 889  |
| Db | 773  | TGTTATCAGGGTCAGGGAGAA-----CTGATTTGTA                             | 802  |
| Qy | 889  | ATGAGCATTTAAAAATGCAAAACGCCAGAGTATACCAATTAATTTGTTTATATTTGGTATCAGG | 948  |
| Db | 803  | ACGAGCGGTTAAAGCGGAAAATAAAGAGATATACAAATTAATTTGTTAGGGTGGTATAAAC    | 862  |
| Qy | 949  | TAGGTTTAAATCAGATAAAAACAGGGGGGACAGGTGCTGACACTTGGTTCGAAATTTAATA    | 1008 |
| Db | 863  | AGGGTTTAGATCAGATAAGACAGCGGGGTACAAGTGTGAAAGTTTGGTTCGAAATTTAATA    | 922  |
| Qy | 1009 | AAATTCGTAGAGAAATGACGTTGGCGGTATTTGGATTTATTCGTATATTTTCCAACTTATG    | 1068 |
| Db | 923  | AAATTCGTAGAGAAATGACGTTGGCGGTATTTGGATTTATTTGCTATATTTTCCAACTTATG   | 982  |
| Qy | 1069 | ATTTTGAGAAATATCCATATGCAACACATGTAGAGTTGACTTAGGGAAATTTATACAGATG    | 1128 |
| Db | 983  | ATTTTGAGAAATATCCATATGCAACACAGTGTAGAGTTTAACTTAGGGAAATTTATACAGATC  | 1042 |
| Qy | 1129 | CAGTGGGATATTCATTCGGGAACCTTATAGTTGGTTTACGGAAATGCGCCTAACTTTTAAATG  | 1188 |

|                          |          |   |      |   |      |
|--------------------------|----------|---|------|---|------|
| D                        | b        |   | 1043 | CAGTGGGATATTACAGGGGGAAATATATGGTTGGGAACGGTTTT-----TAGCTTTAATT      | 1096 |
| Q                        | y        |   | 1189 | GTTTAGAGGCTTAATGGNAACCGGGACCTGGTTTAGTTACTTCGGCTAGCCAAATAGGTA      | 1248 |
| D                        | b        |   | 1097 | CGGTAGAAGCAAAATGGAACACGGGGACCTGGTTTAGTTACTTCGGCTTCAAAGCTATAGATA   | 1156 |
| Q                        | y        |   | 1249 | TATATAATGAGTATGTT-----TCGAGATATATTTGCCGGCTGGGTAGGAACCTCGTC        | 1299 |
| D                        | b        |   | 1157 | TATATAGTCATTCTATTAACTTCACGCTTGTTATCTTAGTGGCTGGGGGGAACCTCGTC       | 1216 |
| Q                        | y        |   | 1300 | ATTATGAAGACTACACAAGGGTAACGGTATTTTTCAACGATATGTCGAACTACCAAGTA       | 1359 |
| D                        | b        |   | 1217 | ATTATGAAGACTTCCACAAGGGTAACGGTGCTTTTCAACGATATGTCGAACTACCAAGTA      | 1276 |
| Q                        | y        |   | 1360 | ATGATCTACCGTATATTTGATTTTCAGAAATGCCGATGATATATAAAATTAATCTCATTTAGCTA | 1419 |
| D                        | b        |   | 1277 | ATAATCACCGTAAATATATTTTTTGGCAATACCGATATATTTAAAAATTAATTTTCATTAGCTA  | 1336 |
| Q                        | y        |   | 1420 | TCATG----AACCTAGTAGGAGAGACTACCGCTAGACACAGAGTATCGTGTTCCTCAAAAGCAG  | 1476 |
| D                        | b        |   | 1337 | GATATGCAATGCAAACCGTTTGTGGGTATTCATCCACGGGATCTTGTTTCACGTGCAG        | 1396 |
| Q                        | y        |   | 1477 | ATTTTCGTAGGGTAGGGGGACCTGATTTTAAATTTATGATCGAGGTAAATAATGGGCTAAGCA   | 1536 |
| D                        | b        |   | 1397 | AAATTTTTCCGACAAACACTAAATACTTTCTCTGTATGAGGTAAACAGTTCTCGGTA--CT     | 1453 |
| Q                        | y        |   | 1537 | GGATGCAAAATGAACTCACTACGTTCCCACCTGTATTTGCACCTCTAA-----TGGTGTTAGAG  | 1590 |
| D                        | b        |   | 1454 | CACAGCAAAATTTGAAATCTGTGTACCAGGTATTAATAAGGATCTACACCTAGTCGTACAA     | 1513 |
| Q                        | y        |   | 1591 | GACCTCTCATAGATTAATCAAAATCGGCGATGTCTGTATATATGGAACCTCCAGAGTTAAACG   | 1650 |
| D                        | b        |   | 1514 | ATTACTCTCATAGTATTAATCAAAATCGGCGATGTCTGTATATGGAACCTCCAGAGTTAAACG   | 1573 |
| Q                        | y        |   | 1651 | TATATGTTGGACACATACAAAGTTTAAAACGTTGAAATATAATTTGAAGCCAATCAAAATTA    | 1710 |
| D                        | b        |   | 1574 | TATTTGGTTGGACACATACAAAGTATGAAAAAAGATTAATCGAATTTATCCAGATAAAATTA    | 1633 |
| Q                        | y        |   | 1711 | CACAAATACCGCGGTGACAGAGTTATACCTTCAAAAATTAATCTTGTCTAATGCTCTACCT     | 1770 |
| D                        | b        |   | 1634 | CGCAAAATTCCTGCAGTAAAGCTTTTGGCCCTACACAGGTACAGGATATGCAGGAGGTT       | 1693 |
| Q                        | y        |   | 1771 | ATGTAATAAAAGGCACCT  | 1787 |
| D                        | b        |   | 1694 | ACGTCACAGCTGGGCT  | 1710 |
| <br>RESULT 7<br>AAN82106 |          |   |      |   |      |
| ID                       | AAN82106 | standard; DNA; 3684 BP.   |      |   |      |
| XX                       | AC       | AAN82106;   |      |   |      |
| XX                       | DT       | 25-MAR-2003 (revised)   |      |   |      |
| DT                       | DT       | 31-OCT-2002 (revised)   |      |   |      |
| DT                       | DT       | 13-NOV-1990 (first entry)                                       |      |   |      |
| XX                       | DE       | Sequence contg. gene encoding Bacillus thuringiensis 8 protein. |      |   |      |
| XX                       | KW       | Bt 8 protein; insecticides; mosquitos; ss.                      |      |   |      |
| XX                       | OS       | Bacillus thuringiensis.   |      |   |      |
| XX                       | FH       | Key Location/Qualifiers   |      |   |      |
| FT                       | RBS      | 145..149  |      |   |      |
| FT                       | FT       | /*tag= b  |      |   |      |
| FT                       | CDS      | 157..3567   |      |   |      |
| FT                       | FT       | /*tag= a  |      |   |      |
| FT                       | FT       | /label= Bt 8 protein  |      |   |      |
| XX                       | FN       | WO8086631-A.  |      |   |      |
| XX                       | XX       |   |      |   |      |



08-MAY-2002 (first entry)

Bacillus thuringiensis variant israelensis toxin (Bt8) gene sequence.

Toxin; Bt8; insecticidal; cyanobacterium; synchocystis 680; endotoxin; mosquito control; glutamine synthetase inhibitor; inoculum; gene; ds.

Bacillus thuringiensis serovar israelensis.

Key Location/Qualifiers  
RBS 145..149  
/\*tag= a  
/standard\_name= "Shine-Dalgarno (SD) Sequence"  
/note= "Consensus ribosome binding site"  
CDS 157..3567  
/\*tag= b  
/product= "Bacillus thuringiensis toxin (Bt8) protein"  
/transl\_except= (pos:1708..1710, aa:Ser)  
/transl\_except= (pos:2356..2358, aa:Gln)  
/transl\_except= (pos:3067..3069, aa:Gln)

US6335008-B1.

01-JAN-2002.

18-FEB-1992; 92US-00837625.

04-MAR-1987; 87US-00021405.

13-SEP-1988; 88US-00243798.

(UNMS ) UNIV MICHIGAN STATE.

Vaeck MA, Chungjatupornchai W, McIntosh L;  
WPI; 2002-163196/21.  
P-PSDB; AAU76029.

Novel chimeric gene expressed in cells of Cyanobacterium for controlling mosquitoes in water, comprises a DNA fragment comprising promoter region and a DNA fragment containing gene encoding for insecticidal protein.

Example 2; Fig 2a; 36pp; English.

The present invention relates to a new chimeric gene expressed in cells of a Cyanobacterium such as Synchocystis 680. The gene comprises a DNA fragment having a promoter region, for expression of a DNA fragment in the Cyanobacterium, and a fragment coding for an insecticidally active protein endotoxin produced by Bacillus thuringiensis, B. ephraemicus or B. kurstaki strain, or for a truncated form of the protein. Cyanobacterium is useful for controlling mosquitoes in water by applying the bacterium to a region to be controlled, where the cyanobacterium which contain and express the bar gene are selectively protected against competing non-transformed Cyanobacteria by treating the region with glutamine synthetase inhibitors. The invention is useful as viable inoculum to settle the regions, especially the swamps and all stagnant waters/ which promote the growth of mosquito larvae. Cyanobacterium provides better control of mosquitoes, ensures a long-term destruction of mosquitoes, guarantees direct uptake of the bacterium by the mosquitoes and assures more stable availability of the toxin in the vicinity surface since it is self replicating and floats at or near the water surface. The present nucleic acid sequence encodes the B. thuringiensis variant israelensis toxin (Bt8) protein of the invention. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 3684 BP; 1301 A; 587 C; 694 G; 1102 T; 0 U; 0 Other;  
Query Match 13.2%; Score 789; DB 6; Length 3684;  
Best Local Similarity 71.3%; Pred. No. 5-2e-134;  
Matches 1092; Conservative 0; Mismatches 415; Indels 24; Gaps 3;

2260 TTACTAGATAGGTGATGCTGTTTAAACAATAAGCGAAAAAGGTTGTGAGTCCTAT 2319  
2064 TGTATTAGATGACACAGAACCAAAATTTAGAAATCAGAACGAGAAGTTGTGAATGCACT 2123

QY 2320 GTTTACAAGTAGTACGAAATAACGTTAAATAATAGAAACGACAGATTATGAATAGATCA 2379  
2124 GTTTACAATAGACGCCGAAAGATGCATTAACATTTGGAACGACAGATTATGACATAGATCA 2183  
2380 AGCGGCCATTTTCTATAGAATGTATGTAGATGAACAAAATCCTCAGGAAAAAATAATGTT 2439  
2184 AGCCGCAATCTTGTGGAATGATTTCTGAAGAATTTATATCCAAAAGAAAAATGCTGTT 2243  
2440 ATGGGATGAATTAATAACTGCGCAAAACAACTTAGTCTAGTCTCGTAATCTACTCCAAATGG 2499  
2244 ATTAGATGAAGTTTAAAAAATGCGAAACAACCTTAGTCAATCTCGAAATGTACTTCAAAACG 2303  
2500 AGACTTTT-----TCGGGAAATGATTGGACATTTCCGTTAATGATTATATCATAGATCCAA 2553  
2304 GGATTTTGAATCGGCTACCGTTGGTGGACAAACAGTGAATAATATCACAATTTGAAGAAGA 2363  
2554 TAATCTTATTTTAAAGGAAAAATTTCTACAGATGCGTGGAGCACGAGACATATATGGAAC 2613  
2364 TGATCCTATTTTAAAGGCAATTACCTTCATATGCTCTGGGCGAGAGACATTGATGGTAC 2423  
2614 TCTATTTCCAACTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAACCATATACACG 2673  
2424 GATATTTCCGACCTATATATTTCCAAAAAATTTGATGAATCAAAATTTAAACCGTATACACG 2483  
2674 TTATCGAGTAAGAGGGTTTGTGGGAAGTAGTAAGGATTTGAAATTAATGTAACACGTTA 2733  
2484 TTACCTAGTAAGGGGATTTGTAGGAAGTAGTAAGATGTAGAACTAGTGGTTTCCGCGTA 2543  
2734 CGGAAAGAAATTTGATGCTATCATGAATGTTCCAAATGATTTGGCCCTATATGACAGCTAA 2793  
2544 TGGGGAAGAAATTTGATGCTCATGAATGTTCCAGCTGATTTAAACTATCTGTATCCTTC 2603  
2794 TCTTTCATGTGGAGATTTGCGTGTGAATCATGCTCTCAGTATGTGAGCCAAAGGGTATCC 2853  
2604 TAC-----CTTTGATTGTGAAGGGTCTAATCGTTGTGAGACGTCCTCGTGGCC 2651  
2854 TACACCAACAGATGGATATGCTCCGATATGATGCATGCCCGCCCAAAATATAGATAGAAA 2913  
2652 GGTAAACATGGGAACACTTCTGATATGTTGTTATTCATGCCAATATGATACAGGGAATA 2711  
2914 GCATGTGAAGTGTACGATCGTCATCCATTTGATTTTCATATTTGACACCGGAGAAGTAGA 2973  
2712 GCATGTCGATGTGAGGATTTCCATCAATTTAGTTTCACTATTTGATACAGGGSCATTAGA 2771  
2974 TACAATACAATGTAGGTATTTGATGCTCTTATTAATAATTTCTTAATCCAGATGGATACGC 3033  
2772 TACAATGAAAAATATAGGGGTTTGGGTCATGTTTAAATATCTTCTCCAGATGGATACGC 2831  
3034 TACAGTAGGGAATCTAGAGTCTATTGAAGAAGGCCACTAACAGGTTGAAGCATTTGGCACA 3093  
2832 ATCATTTAGTAATTTTAGAAGTAATTTGAAGAAGGCCAATAGATGGGGAAGCATGTGCACG 2891  
3094 TGTGAAACAAAAAGGAAAAAGAAATGGAACAACACATGGAGAAAAAACGTTGGGAAAAACACA 3153  
2892 CGTGAACACATGGAGAGAAATGGAACCATCAATGGAAGCAAAACGTTTCGGAACACACA 2951  
3154 ACAAGCTATGATCCAGCAAAAACAGGCTGTAGATGCATTTATTTACAATTTGAACAAGA--- 3210  
2952 ACAAGCATATGATGTAGCGAAAACAAGCCATTGATGCTTTTATTCACAAAATGTACAAGATGA 3011  
3211 ---GTTACACTATCATTTTACTTTTATAGATCATATTCAAAACGCTGATCGACTGTACAGTC 3267  
3012 GGGTTTACAGTTTGTATACACACACTCGCTCAAAATTCAGTACGCTAGTATTTGGTGCATC 3071  
3268 GATTCCTATGTATACCAATAATTTGGTTTACCGAATGCTCCAGGTATGAACTATGATGTATA 3327  
3072 GATTCATATGTGTACAAATGATTTGGTTGTCAGATGTTCCAGGTATGAATTTATGATATCTA 3131  
3328 TCAAGAGTTAAACGACACGTATCATGCAAGTTTATTAATTTATGATGACGAATGTCAT 3387  
3132 TGTAGAGTTGGATGACACAGTGGCAACAGCGGTTTATTTGTTATGATACAGAATAATTAT 3191





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Qy 3034 TACAGTAGGAATCTAGAAGTCATTGAAGAGGACCACTAACAGGTGAAGCATTTGGCACA 3093
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3832 ATCAATTAGATAATTTAGAGGTAAATTGAAGAGGGCCAAATAGATGGGGAAGCACTGTCAAG 2891
Qy 3094 TGTGAACAAAGGAAAGAAATGGAACCAACACATCGAGAAATAAAAGCTTTGGGAAACACA 3153
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2892 CGTGAACACATGGAGAGAAATGGAACGATCAATGGAAGCAAAAGCTTCGGAAACACA 2951
Qy 3154 ACAAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTTTACAAATGAACAAGA- -- 3210
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2952 ACAAGCATATGATGTAGCGAAACAGGCCATTGATGCTTTATTCACAAATGTACAAGATGA 3011
Qy 3211 ---GTTACATCATATTACTTTAGATCATATTTCAAACGCTGATCGACTGGGTACAGTC 3267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3012 GGGCTTACAGTTTATACGACACTCGCTCAAAATTCAGTACGCTGAGTATTTGGTACAATC 3071
Qy 3268 GATTCCCTATGTATACCAATTAATGGTTACGAATGCTCCAGGTATGAACTATGATGTATA 3327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3072 GATTCCATATGTGTACAAATGATTTGGTTGTGAGATGTTCCAGGTATGAATTTATGATATCTA 3131
Qy 3328 TCAAGAGTTAAACGACGCTATCATGCAAGGTTTATAATTTATATGATGCACGAATGTGAT 3387
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3132 TGTAGAGTTGGATGACAGGTGGCAACAGCGGTTATTTGATGATACAAAGAAATATAT 3191
Qy 3388 AACAAATGGTGACTTTACAAAGGATTAACAGGATGGCACGCAACAGAAATGCCGCGT 3447
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3192 TAAAAATGGTGATTTTACAAAGGGGTAATGGGGTGGCATGTAACCTGGAATGCAGACGT 3251
Qy 3448 ACAACAAATCGATGGAGCTTCAGTATTTAGTTCTATCAAAATTTGGAGCGCGGGGTATCTCA 3507
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3252 ACAACAAATAGATGGTGTTTCTGTATTTGGTTCTATCTAATTTGGAGTGCTGGCGTATCTCA 3311
Qy 3508 AAACCTTGCACTGCTCAAGATCATCATGATGATGTGTTACGTTGATTTGCCAAAGAAAGG 3567
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3312 AAATGTCCTCTCAACATTAATCATGGGTATGCTTACGTTGATTTGCCAAAGAAAGG 3371
Qy 3568 ACCTGGAAGAGGTATGTAAACGATGATGGAATTTGTAATGGAAGCAGGAAACACTTAAGTT 3627
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3372 ACCTGGAATGGGTATGTGTCAGCTTATGCGTTTGTGAGGAGAAATCAAGAAATTTGAGTT 3431
Qy 3628 CACTTCTTGGAAGAGGATATATGACAAACACAGTAGAGGTATTTCCGAAAGATGATCG 3687
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3432 TAGCTCTTGGAAGAGGATATATACGAACAGATAGATGTATTTCCAGATACAGATCG 3491
Qy 3688 TGTACGGATTTGAATAGGAGAAACCGAAGGTACATTTTATATAGATAGCATCGATTGCT 3747
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3492 TGTACGAATTTGATAGTGGCGAAACCGAAGGTTTCGTTTTATATCGAAAGCATTTGAATTAAT 3551
Qy 3748 TTGTATGCAAGGATATGATTAACAAATTAATAC 3778
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3552 TTGCATGAACGAGTGATTAATAAAATAAC 3582
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## RESULT 10

AAN92515  
ID AAN92515 standard; DNA; 4065 BP.

XX AC AAN92515;

XX DT 25-MAR-2003 (revised)

DT 23-DEC-1990 (revised)

DT 15-MAY-1990 (first entry)

XX DE Sequence of insecticide gene from *Bacillus thuringiensis israelensis* strain.

XX KW Insecticide; diptera larvae; aedes; ss.

XX OS *Bacillus thuringiensis*.

XX FT Key Location/Qualifiers  
CDS 461..3868  
/\*tag= a

XX JP01080294-A.  
PN 27-MAR-1989.  
XX 21-SBP-1987; 87JP-00238394.  
XX 21-SBP-1987; 87JP-00238394.  
XX (SUMO) SUMITOMO CHEM IND KK.  
PA (MARU-) MARUBENI KK.  
XX WPI; 1989-134798/18.  
DR P-PSDB; AAP93308.  
XX Insecticide protein gene - from *Bacillus thuringiensis israelensis* strain, used to produce protein toxic to diptera larvae, eg. aedes.  
XX Fig 2; Fig 2-1 to 2-3; 8pp; Japanese.

CC The protein gene has high insecticide activity to diptera larvae such as aedes. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 4065 BP; 1471 A; 595 C; 752 G; 1247 T; 0 U; 0 Other;

Query Match 13.2%; Score 789; DB 1; Length 4065;  
Best Local Similarity 68.0%; Pred. No. 5.3e-134;  
Matches 1171; Conservative 0; Mismatches 520; Indels 30; Gaps 4;  
Qy 2292 AATAAGCGAAAGGTTGTGAGTCCCTATGTTTACAAGTAGTAGCGAAAAATACGTTAAAAA 2351  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2277 AATCAGAACGAGAAGTTGTGAATGCACTGTTTACAATGACGCGAAGATGCATTAAACA 2336  
Qy 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGTATGTCAGATG 2411  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2337 TTGGAACGACAGATTATGACATAGATCAAGCGCCAAATCTTGTGGAATGTATTTCTGNAAG 2396  
Qy 2412 AACAAAATCCTCAGGAAATAATGTTATGGATGAAATAAACTGCGCAAAACAACTTA 2471  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2397 AATTATATCAAAAGAAATAATGCTGTTATAGATGAAATTAATAATGCGAAACAACTTA 2456  
Qy 2472 GTCAGTCTGTAATCTACTCCAAAATGGAGACTTT-----TCTGGGAATGATGGACAT 2525  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2457 GTCAATCTCGAATGTACTTCAAAACGGGATTTTGAATCGGCTACGCTTGGTTGACAA 2516  
Qy 2526 TCGGTAATGATATATCATAGGATCCAATTAATCTTATTTTAAAGAAATTTCTACAGA 2585  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2517 CAAGTGATAATATCACAATTCAGAAGATGATCCTATTTTAAAGGCGATTACCTTCATA 2576  
Qy 2586 TCGGTGAGCAGACATATATGGAATCTTATTTCCAACTATATCTGTCAAAAATAG 2645  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2577 TGTCTGGGCGAGAGACATTTGATGGTACGATATTTCCGACCTATATATTTCCAAAAAATTG 2636  
Qy 2646 ATGAGTCTAAATTAACCAATATACACGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 2705  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2637 ATGAATCAAAATTAACCGTATACAGTTTACCTAGTAGGGGATTTGTAGGAAGTAGTA 2696  
Qy 2706 AAGATTGAAATTAATGGTAAACAGTTACGGGAAAGAAATGATGCTATCATGAATGTTTC 2765  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2697 AAGATGTAGAACTTAGTGGTTTCACTGATGGGAAAGAAATGATGTCATCATGAATGTTTC 2756  
Qy 2766 CAAATGATTTGGCCTATATGACGCTTAATCTTCACTGCGAGATTAATCGCTGTAATCAT 2825  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2757 CAGCTGATTTAAACTATCTGTTCTTCTACCTTTGAT-----TGTGAAGGGT 2804  
Qy 2826 CGTCTCAGTATGTGAGCCAAAGGTTATCTTACACCAACAGATGATATGCTCCCGATATGT 2885  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2805 CTAATCGTTGTGAGCGTCCGCTGTCGCGCTTAACTTGGGAACACTTCTGATATGTTGT 2864  
Qy 2886 ATGCATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTGACGATCGTCATCCATTTG 2945  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
2865 ATTCATGCCAATATGATACAGGGAAGAAAGCATGTCGTATGTCAGGATTTCCCATCAATTA 2924



Db 2148 GGATTTTGAATCGGCTACGCTTGGTGGCAACAAAGTGATAATATCAAAATTCAGAAGA 2207  
 Qy 2554 TAATCCCTATTTTAAAGGAAATTTCTACAGATCGGTGGACGACGACATATATGAAC 2613  
 Db 2208 TGATCCCTATTTTAAAGGCAATTAACCTTCATATGCTCGGGCGGAGACATTTGATGGTAC 2267  
 Qy 2614 TCTATTTCCAACTTATCTGTCAAAAATATAGATGAGTCTAAATTTAAAAACCATATACACG 2673  
 Db 2268 GATATTTCCGACCTATATATTCACAAAAATTTGATGAATCAAAATTTAAAAACGATATACACG 2327  
 Qy 2674 TTATCGAGTAGAGAGGTTTGGGAAGTAGTAAGATTTGAAATTAATAGTTAAACAGCTTA 2733  
 Db 2328 TTACTAGTAAGGGGATTTGTAGGAAGTAGTAAGATTTGAAATTAATAGTTAAACAGCTTA 2387  
 Qy 2734 CGGGAAGAAATTCATCTCATGAATTTTCCAAATGATTTGGCCTATATGACAGCCTAA 2793  
 Db 2388 TGGGAAGAAATTCATGCGCATCATGAATTTTCCAGCTGATTTAACTATCTGTATCTTC 2447  
 Qy 2794 TCCTTCATGTGGAGATTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAAGGGTATCC 2853  
 Db 2448 TAC-----CTTTGATTGTGAAGGCTCTAAATCGTTGTGAGACGTCGCTGTGCC 2495  
 Qy 2854 TACACCAACAGATGATATGCTCCCGATATGATATGATGCGCGCAAAATATAGATAGAAA 2913  
 Db 2496 GGCTAACATTGGGAACACTTCTGATATGTTGATTTTCATGCAATATGATACAGGGAAAAA 2555  
 Qy 2914 GCATGTGAAGTGTCAAGATCGTCAATTTGATTTTTCATATGACACCGGAGAGTAGA 2973  
 Db 2556 GCATGTGATGTGAGGATTTCCCATCAATTTAGTTTCACTATGATACAGGGGATTAGA 2615  
 Qy 2974 TACAAATPACAAATGTAGTATTTGATGCTTTTAAATAATTTCTAAATCCAGATGGATACGC 3033  
 Db 2616 TACAAATGAAAAATATAGGGTTTGGGTGATGTTTAAATAATTTCTCCAGATGGATACGC 2675  
 Qy 3034 TACAGTAGGAATCTAGAGTCAATTGAAGAGGACCACTAACAGGTGAAGATTTGGCACA 3093  
 Db 2676 ATCATTAGATAAATTTAGAGTAATTTGAAGAGGGCCAAATAGATGGGGAAGCACTGTCA 2735  
 Qy 3094 TGTGAACAAAGGAAAGAAATGGAACCAACATCGAGGAAAGAAAGCTTTGGGAAACACA 3153  
 Db 2736 CGTGAACACATGGAGAAGAAATGGAACGATCAATGGAAGCAAAAGCTTTGGGAAACACA 2795  
 Qy 3154 ACAAGCCTATGATCAGCAAAAACAGGCTGTAGATGCAATTTTACAAATGAAACAAAGA-- 3210  
 Db 2796 ACAAGCATATGATGACGGAACCAAGCCATTGATGCTTTTACAAATGTAACAGATGA 2855  
 Qy 3211 ----GTTACACTATCATATTTCTTAGATCATATTTCAAAAACGCTGATGCACTGGTACAGTC 3267  
 Db 2856 GGCTTTACAGTTTGATACGACACTCGCTCAAAATTCAGTACGCTGAGTATTTGGTACAAATC 2915  
 Qy 3268 GATTTCCCTATGATACCATTAATTTGTTTACCGAATGCTCCAGGTATGAACTATGATGATA 3327  
 Db 2916 GATTTCCATATGTTACAAATGATGTTGTTGATGATGTTTCCAGGTATGAAATTTATGATATCTA 2975  
 Qy 3328 TCAAGAGTTTAAACGACATCATGCAAGGTTTAAATTTATATGATGACGAAATGTCAT 3387  
 Db 2976 TGTAGAGTTGATGACGAGTGGCACAAGCGCTTATTTGTATGATACAGAAATATAT 3035  
 Qy 3388 AACAAATGGTGACTTTACACAGGATTTACAGGATGGCAGCAACAGAAATGCCGGGT 3447  
 Db 3036 TAAAAATGGTGATTTTACACAAAGGGGTAATGGGGTGGCATGTAACTGGAATTCAGACGT 3095  
 Qy 3448 ACAACAAATGGATGGACCTTCAGTATTTAGTTTCTATCAAAATTTGAGCGGGGTATCTCA 3507  
 Db 3096 ACAACAAATAGATGGTGTCTGTATTTGGTTTCTATCTAAATTTGAGGTGCTGGCGTATCTCA 3155  
 Qy 3508 AAACTTGCATCTCAAGATCATCATGATATGTTTACGTGTGATTTGCCAAAAAAGAGG 3567  
 Db 3156 AATGTCCATCTCCAACATATCATGGGTATGTTTACGTGTTTATTTGCCAAAAAAGAGG 3215  
 Qy 3568 ACTTGGAAAAAGGATGATGAACGATGATGATTTGATTTGAAAGCAGGAAACACTTAAGTT 3627  
 Db 3216 ACCTGGAATGGGTATGTCAGCTTATGGAATTTGAGGAGAAATCAAGAAAAATTTGACGTT 3275

Qy 3628 CACTTCTTGCAGAGGATATATGACAAAAACAGTAGAGTATTTCCAGAAAGTATCG 3687  
 Db 3276 TAGCTCTTGTGAAGAGGATATATACGAAGACAGTAGATGTATTTCCAGATACAGATCG 3335  
 Qy 3688 TGTACGATTTGAAATAGGAGAAACCGAAGCTACATTTTATATAGATAGCATCGAGTTGCT 3747  
 Db 3336 TGTACGAATTTGAGATAGGCGAACCAGAGGTTCTGTTTATATCGAAGCATTTGAATTAAT 3395  
 Qy 3748 TTGTATGCAAGGATATGATTAACAATATAAAC 3778  
 Db 3396 TTCATGAACGAGTGAATTAATAAAAAATACC 3426

RESULT 12

AAN96139  
 ID AAN96139 standard; DNA; 4184 BP.  
 XX  
 AC AAN96139;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 15-MAY-1990 (first entry)  
 XX  
 DE Bacillus thuringiensis israelis strain toxin.  
 XX  
 KW Bacillus thuringiensis, israelensis strain; toxin; diptera larvae; aedes.  
 XX  
 OS Bacillus thuringiensis; israelensis.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 461..3867  
 FT /\*tag= a  
 FT /\*product= "toxin"  
 XX  
 PN JP01080294-A.  
 PD 27-MAR-1989.  
 XX  
 PF 21-SEP-1987; 87JP-00238394.  
 XX  
 PR 21-SEP-1987; 87JP-00238394.  
 XX  
 PA (SUMO ) SUMITOMO CHEM IND KK.  
 PA (MARU-) MARUBENI KK.  
 XX  
 DR WPI; 1989-134798/18.  
 DR P-PSDB; AAP93308.  
 XX  
 PT Insecticide protein gene - from Bacillus thuringiensis israelensis  
 PT strain, used to produce protein toxic to diptera larvae, eg. aedes.  
 XX  
 PS Fig 2(1) - 2(3); pages 639-40; 8pp; Japanese.  
 CC The gene is used to produce protein toxic to diptera larvae, e.g. aedes.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated  
 CC on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 4184 BP; 1501 A; 627 C; 774 G; 1282 T; 0 U; 0 Other;

Query Match 13.1%; Score 781.8; DB 1; Length 4184;  
 Best Local Similarity 68.2%; Pred. No. 1.1e-132;  
 Matches 1173; Conservative 0; Mismatches 517; Indels 31; Gaps 5;  
 Qy 2292 AATAACCGAAAAAGGTTGTGAGTCCCTATGTTTACAAAGTAGTAGCAAAAAATACGTTAAAAA 2351  
 Db 2397 AATCAGAACGAGAGTTGTGAATGCACTGTTTACAATGACGCAAGATGCAATTAAACA 2456  
 Qy 2352 TAGAAAACGACAGATTATGAAATAGATCAAGCGGCCCAATTTCTATAGAAATGTATCTCAGATG 2411  
 Db 2457 TTGGAACGACAGATTATGACATAGATCAAGCCGCAAAATCTTGTGGAATGTATTCTTCTGAAG 2516



PT gene library from plasmid deoxyribonucleic acid, etc.

XX Disclosure; Page ?; 9pp; Japanese.

XX A plasmid contg. the gene is isolated by forming a gene library from  
CC plasmid DNA of *B. thuringiensis israelensis* (HD 522 strain, USA Goldberger  
CC ONR60) followed by screening with anti-*israelensis* insecticidal protein  
CC IG. The insecticidal protein is highly effective against *Diptera*, esp.  
CC *Aedes*. (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 4934 BP; 1797 A; 749 C; 877 G; 1511 T; 0 U; 0 Other;

Query Match 13.0%; Score 774.6; DB 1; Length 4934;

Best Local Similarity 71.4%; Pred. No. 2.2e-131;

Matches 1071; Conservative 0; Mismatches 404; Indels 24; Gaps 3;

QY 2292 AATAAGCGAAAAAGGTTGTGAGTCTATGTTTACAGTAGTACGAAAAATACGTTAAAAA 2351

DB 3440 AACAGGTACAAACAATAATTAACATTTTATGCAATCTTATAAAAAACACTTTACAAT 3499

QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCAATTTCTATAGATGTATGTCAGATG 2411

DB 3500 CAGAACTTACAGATTATGACATAGTACGCCGCAATCTTGTGGAATGTATTTCTGAAG 3559

QY 2412 AACAAAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471

DB 3560 AATTATATCCAAAAGAAAAAATGCTGTTATTAGATGAAGTTAAATAATGCCGAACAACTTA 3619

QY 2472 GTCACTCTGTAATCTACTCAAAAATGGAGACTTT-----TCGGAATGATGGACAT 2525

DB 3620 GTCAATCTCGAAATGTACTTCAAAACGGGGATTTTGAATCGGCTACGCTTGGTTGGACAA 3679

QY 2526 TCGGTATGATATTATCATAGGATCCAAATATCTATTTTCCAACTTATCTGTCAAAAAATAG 2645

DB 3680 CAAGTATATATCACAATTCAGAGATGATCTATTTTAAAGGGCATTCCTTCATA 3739

QY 2586 TCGGTGAGACAGACATATATGGAATCTATTTTCCAACTTATCTGTCAAAAAATAG 2645

DB 3740 TGTCTGGCGGAGACATTTGATGGTACGATATTTCCGACCTATATATTCNAAAAATG 3799

QY 2646 ATGAGTCTAAATTAACCAATATACAGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 2705

DB 3800 ATGAATCAAAATTAACCAATATACAGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 3859

QY 2706 AAGATTGAAATTAATGTTAAACAGTTTACCGGAAAGAAATTTGATGTCATCATCAATCTTC 2765

DB 3860 AAGATGTAGAACTAGTGTTTACGCTATGGGGAAGAAATTTGATGTCATCATCAATCTTC 3919

QY 2766 CAAATGATTTGGCTTATATGACGCTTAATCTTTCATGTGGAGATTATCGCTGTGAATCAT 2825

DB 3920 CAGCTGATTTAAACTATCTGATCTTCTAC-----CTTTGATTTGGAAGGT 3967

QY 2826 CGTCTCGATGTGAGCGCAAGGGTATCTCTACACCAACAGATGGATATGCTCCCGATGT 2885

DB 3968 CTAATCGTTGTGAGACGCTCGCTGTGCGGCTAACATTTGGGAACACTTCTGATATGTTGT 4027

QY 2886 ATCAGTCCCGCAAAATATAGTAGAAGCATGTGAAGTGTACAGTGTGTCATCTCCATTG 2945

DB 4028 ATTCTGCCCAATATGATACAGGGAAGAAAGCATGTGATGTCAGGATTCCTCAATTA 4087

QY 2946 ATTTTCATATTGACCCGGAAGATGATAGATACAAAATGAGTATGATGTTGATCTTAT 3005

DB 4088 GTTTCATATTGATACAGGGCATTTAGATACAAATGAAATATAGGGGTTTGGGTATGT 4147

QY 3006 TAAAAATTTCTAATCCAGATGGATAGCTACAGTAGGGAATCTAGAGTCATTGGAAG 3065

DB 4148 TTAATAATATCTTCCAGATGGATAGCGCATTTAGATTAATTTAGAAATTTGAAGAAG 4207

QY 3066 GACCACTTAACAGGTGAAGCATTCGCACATGTGAAACAAAGGAAGAAATGGAACAC 3125

DB 4208 GGCATATAGATGGGAAGCACTGTCCGCTGAAACACATGGGAAGAAATGGAACATC 4267

QY 3126 ACATGGAGAAAAACGTTGGGAAACACAAACGCTTATGATCCAGCAAAACAGGCTGTAG 3185

DB 4268 AATGGAGCAAAACGTTTCGAAACACAAACGATATGATGTAGCGAAACAGCCATTG 4327

QY 3186 ATGCAATTATTCAAAATGAACAAG-----GTTACACTATCATATTACTTTAGATCAT 3239

DB 4328 ATGCTTTATTTCACAAATGTACAAGATGAGGCTTTACAGTTTGTATACGACACTCGCTCAAA 4387

QY 3240 TTCAAAACGCTGATCGACTGGTACAGTCGATCCCTATGTATACCATTAATTTGGTTACCGA 3299

DB 4388 TTCAGTACGCTGAGTATTTGGTACAATCGATTCCATATGTGTACAATGATTTGGTTGCAG 4447

QY 3300 ATGCTCCAGGTATGAATGATGATATCAAGAGTTTAAACGCAACGCTTATCATGCAAGGTT 3359

DB 4448 ATGTTCCAGGTATGAATATGATATCTATGAGTGGTATGACGAGTGGCAACAGCGC 4507

QY 3360 ATAAATTTATGATGACACGAAATGTCAACAATAATGTTGATCTTTACAAAGGATTTACAGG 3419

DB 4508 GTTATTTGTATGATCAAGAATAATTTATTTAAAAATGTTGATTTTACACAAGGGGTAAATGG 4567

QY 3420 GATGGCAGCAACAGGAAATGCCCGGTACAACAAATGGATGGAGCTTCAGTATTAGTTTC 3479

DB 4568 GGTGGCATGTAACTGGAAATGACAGCGTACAACAAATAGATGGTGTCTGTATTGGTTTC 4627

QY 3480 TATCAAAATGGAGCGCGGGGTATCTCAAAACCTTGCATGCTCAAGATCATCATGGATATG 3539

DB 4628 TATCTAATTTGGAGTGTGCGGTATCTCAAAATGTTCCATCTCCAAACATTAATCATGGGTATG 4687

QY 3540 TGTATCGTGTATGTCACAAAAGAGGACCTGGAAAAAGGTTATGTAACGATGATGGATT 3599

DB 4688 TCTTACGTTGTTATGTCACAAAAGAGGACCTGGAAATGGGTATGTGACGCTTATGGATT 4747

QY 3600 GTAAATCGAAGCAGGAAACACTTAACTTCACTTCTTTCGCAAGAGGATATATACAAAAA 3659

DB 4748 GTGAGGAGAAATCAAGAAAAATTTGACCTTTTGTGAAGAGGATATATATACGAAGA 4807

QY 3660 CAGTAGAGGTATTTCCAGAAAGTATGCTGTACGGATTGAAATAGGAGAAACCGAAGGTA 3719

DB 4808 CAGTAGATGTATTTCCAGATACAGATCGTGTACGAATTTGATAGGCGAAACCGAAGGTT 4867

QY 3720 CATTTTATATAGATACATCGAGTTGCTTTGTTATGCAAGGATATGATAAATAAATAAC 3778

DB 4868 CGTTTTATATCGAAAGCATTTGAATTAATTTGTCATGAACGAGTGAATTAATAAAAAATAAC 4936

RESULT 14

AAQ81178 standard; DNA; 3543 BP.

XX AAQ81178;

XX AC AAQ81178;

DT 25-MAR-2003 (revised)

DT 12-AUG-1995 (first entry)

XX B.t. toxin PS71M3 gene.

XX Delta-endotoxin; crystal protein; biological control agent; Calliphorid;

XX screw-worm; sheep blowfly; Lucilla; Phormia; Calliphora; insecticide;

XX pesticide; B.t.; ss.

XX Bacillus thuringiensis.

XX WO9502694-A2.

XX 26-JAN-1995.

XX 13-JUL-1994; 94WO-US007902.

XX 15-JUL-1993; 93US-00093199.

XX (MYCO ) MYCOGEN CORP.

XX Hickie LA, Payne J;

XX PI

DR WPI; 1995-067338/09.  
DR P-PSDB; AAR63078.  
XX Method for controlling Calliphoridae pests - specifically utilises  
PT Bacillus thuringiensis isolates or toxins.  
XX  
XX  
PS Disclosure; Page 36-38, 50pp; English.  
XX  
CC A library was constructed from *Bacillus thuringiensis* PS71M3 total  
CC cellular DNA in lambda Gem-11. plasmid pMYC1625, selected in *Escherichia*  
CC coli, contained a 8.0 kb insert expressing a beta-endotoxin gene. This  
CC was sequenced (AA081178). A cured, acrystatalliferous B.t. host carrying  
CC pMYC1625 produced a 130 kDa crystal protein (AAR63078) toxic to  
CC calliphorids. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 3543 BP; 1278 A; 566 C; 612 G; 1087 T; 0 U; 0 Other;  
Query Match 12.8%; Score 765.8; DB 2; Length 3543;  
Best Local Similarity 71.5%; Pred. No. 8.7e-130;  
Matches 1058; Conservative 0; Mismatches 397; Indels 24; Gaps 3;  
QY 2292 AATAACGCGAAAGGTTGTGAGTCTTATGTTTACAAAGTAGTACGAAATACGTTAAAAA 2351  
DB 2072 AACAGTACACAAATTAATACATTTTATGCAATCTTAAACACCTTTACAT 2131  
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATPAGAAATGTATGTCAGATG 2411  
DB 2132 CAGAACTTACAGATTATGACATAGATCAAGCGGCAAACTTTGTGGAATGTATTTCTGAAG 2191  
QY 2412 AACAAATCTCAGGAAATTAATCTTATGGATGAAATTAACCTGGCAACACCTTA 2471  
DB 2192 AATTATATCAAAAGAAATATGCTGTATTAGTGAAGTTAAATATGCGAAACAACTTA 2251  
QY 2472 GTCAGTCTGTAATCTACTCCAAATGGAGACTTT-----TCTGGGAATGATTGGACAT 2525  
DB 2252 GTCAATCTCGAATGTACTTCAAAACGGGATTTTGAATCGGCTAGCTTTGGTTGACAA 2311  
QY 2526 TCGGTAATGATATTATCAGGATGCAATTAATCCTATTTTAAAGGAAATTTCTACAGA 2585  
DB 2312 CAAGTGATAATATCACAATTCAGAAAGATGATCCTATTTTAAAGGCAATACCTTTCATA 2371  
QY 2586 TCGCTCGACGACAGACATATATGGAACCTATTTCCAACTTATCTGTCAAAATATAG 2645  
DB 2372 TGTCTGGGGCGAGAAATTTGATGGTACGATATTTCCGACCTATATATTTCCAAATATG 2431  
QY 2646 ATGAGTCTAAATTTAAACCATATACACGTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 2705  
DB 2432 ATGAATCAAAATTTAAACCGTATACACGTTTACCTAGTAAAGGATTTGTAGGAAGTAGTA 2491  
QY 2706 AGATTGAAATTAATTTGGTAAACAGTTTACGGAAGAAATTTGATGCTATCATGAATGTTTC 2765  
DB 2492 AAGATGTAGAACTAGTGGTTTTCACGCTATGGGGAAGAAATTTGATGCGCATCATGAATGTTTC 2551  
QY 2766 CAAATGATTTGGCTATATGACGCTTAATCTTTCATGTGGAGATTATCGCTGGAATCAT 2825  
DB 2552 CAGCTGATTTAAACTATCTGATCTTCTTAC-----CTTTGATTTGGAAGGTT 2599  
QY 2826 CGTCTCAGTATGTAGCCAGGATATCTTACACCAACAGATGATATGCTCCGATATGT 2885  
DB 2600 CTAATCGTTGTGAGCGCTCGCTGCGGCTAACATTTGGAAACATCTCTGATATCTCGT 2659  
QY 2886 ATGCATCGCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACAGATCGTATCCATTTTG 2945  
DB 2660 ATTCATGCAATATGATACAGGGAAGAAAGCATGTCTGATGTCCAGGATTTCCATCAATTTA 2719  
QY 2946 ATTTTCATTTGACCGGAGAGTAGATACAAATCAAAATGATGATGATGATGATGATGAT 3005  
DB 2720 GTTTTCATTTGATACAGGGGCAATAGATACAAATGAAATATAGAGGTTTGGGTCATGT 2779  
QY 3006 TAAAAATTTCTAATCCAGATGGATAGCTACAGTAGGGAATCTPAGAAAGTCATTTGAAGAAG 3065  
DB 2780 TTAATAATCTTCTCCAGATGGATACGCATCATTAGATTAATTTAGAAAGTAATTTGAAGAAG 2839

QY 3066 GACCACTAACAGGTGAAGCATTTGGCACAATGTGTAACAAAGAAAGAAATGGAACAAAC 3125  
DB 2840 GGCCCAATAGATGGGAAGCACTGTCA CGCTGCAACACATGGAAGAAATGGAACGATC 2899  
QY 3126 ACATCGAGAAAGAAAGCTTTGGGAAACACAAACAGCCCTATGATCCAGCAAAACAGGCTGTAG 3185  
DB 2900 AAATGGAAGCAAAACGTTCCGGAACACAAACAGCATATGATGCGGAACCAAGCCATTA 2959  
QY 3186 ATGCAATTTATTTACAAATGAAACAAGA-----GTTACACTATCATATTTACTTTAGATCAT 3239  
DB 2960 ATGCTTTTATTTACAAATGTACAAAGATAGGCTTTTACAGTTTGATACGACACTCGCTCAA 3019  
QY 3240 TTCAAAACGCTGATCGATCGTGTACAGTGTATCCCTATGATATACCATTAATTTGTTACCGA 3299  
DB 3020 TTACAGTACGCTGAGTATTTGGTACAAATCGATTTCCATATATGTGTACAATGATTTGTTGT 3079  
QY 3300 ATGCTCCAGGTATGAACATGATGATATATCAAGAGTTAAACGACGATCATGTGCAAGGTT 3359  
DB 3080 ATGTTCCAGGTATGAATTTATGATATCTATGTAGATTGGATGCAAGGTCGACAAAGCGC 3139  
QY 3360 ATAAATTTATGATGACGAAATGTCTATAACAAATGGTGACTTTTACACAAAGGATTTACAGG 3419  
DB 3140 GTTATTTGTATGATACAGAAATATTTATTAATAATGGTGATTTTACACAAAGGGTAAATGG 3199  
QY 3420 GATGCAACGCAACAGAAATGCGCGGTACAAACAAATGGATGGAGCTTTCAGTATTTAGTTTC 3479  
DB 3200 GGTGGCATGTAACTGGAATGCGAGACGTACACAAATAGATGGTGTCTCTGTATTTGGTTTC 3259  
QY 3480 TATCAAAATGGAGCGCGGGGTATCTCAAAACTTCGATCTCAAGATCATCATGATGATG 3539  
DB 3260 TATCTAATTTGGAGTCTGCGGTATCTCAAAATGTCATCTCCACATTAATCATTTGGTATG 3319  
QY 3540 TGTACGTGTGATTTGCCAAAAAGAGGACCTGGAAAAAGGTTATGTAACGATGATGATTT 3599  
DB 3320 TCTTACGTGTTATTTGCCAAAAAGAGGACCTGGAAAAAGGTTATGTCAGCTTATGGATT 3379  
QY 3600 GTAATGGAAGCAGAAACACATTAAGTTTCACTTCTTTGGGAAGAGGATATATGACAAAAA 3659  
DB 3380 GTGAGGAGAAATCAAGAAATTTGACGTTTACGCTCTGTGAAGAGGATATATTTACAAAGA 3439  
QY 3660 CAGTAGAGTATTTCCAGAAAGTGTGCTAGCGGATTTGAAATAGGAAACCGAAGGTA 3719  
DB 3440 CAGTAGATGATTTCCAGATACAGATCGTGTACGAATTTGAGATAGCGGAAACCGAAGGTT 3499  
QY 3720 CATTTTATATAGATAGCATCGAGTTGCTTTTGTATGCAAG 3758  
DB 3500 CGTTTATATCGAAAGCATTTGAATTTTGCATGAACG 3538  
RESULT 15  
AAQ14669  
ID AAQ14669 standard; DNA; 3543 BP.  
XX AC AAQ14669;  
XX AC  
XX AC  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 04-FEB-1992 (first entry)  
XX XX  
DE Dipteran active toxin gene.  
XX  
KW Insecticide; B.t; crystal; delta endotoxin; cryIIA; 88.  
XX  
OS *Bacillus thuringiensis* serovar morrisoni.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3543  
FT /\*tag= a  
XX  
XX EP457498-A.  
XX  
PD 21-NOV-1991.  
XX



PF 09-MAY-1991; 91EP-00304180.  
XX 15-MAY-1990; 90US-00524255.  
PR 01-OCT-1990; 90US-00590903.  
XX (MYCO ) MYCOGEN CORP.  
PA Sick AJ;  
PI  
XX WPI; 1991-341902/47.  
DR P-PSDB; AAR14373.  
XX  
XX Bacillus thuringiensis genes encoding diptera-active toxins - and  
PT transformed microbes used to control insects in various environments.  
XX  
XX Claim 1; Page 10; 20pp; English.  
XX  
CC The sequence was obtd. from plasmid pMYC1625 which was isolated from a  
CC genomic library prepd. from DNA from B.t. PS71M3 [from B.t. PS71M3-69  
CC (NRRL B-18515)]. It is related to the cryIVA family of genes, the 140 kD  
CC endotoxin gene and the type II gene from B.t. var. israelensis. The gene  
CC encodes a 130 kD protein. Microorganisms transformed with the DNA may be  
CC administered to dipteran insects or their environments, the expressed  
CC toxins acting as an insecticide. See also AAQ14670-Q14672. (Updated on 25  
CC -MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 3543 BP; 1278 A; 567 C; 612 G; 1086 T; 0 U; 0 Other;

Query Match 12.8%; Score 764.2; DB 2; Length 3543;  
Best Local Similarity 71.5%; Pred. No. 1.7e-129;  
Matches 1057; Conservative 0; Mismatches 398; Indels 24; Gaps 3;

QY 2292 AATAAGCGAAAGGTTGTGAGTCCTATGTTTACAGTAGTACGAAATAACGTTAAAAA 2351  
DB |||||  
QY 2072 AACAGTACCAACAAATAAATAACATTTTATGCAATCTTAAAAAACAACATTTACAAT 2131  
DB |||||  
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTCTCTATAGAAATGATGTGACAGTG 2411  
DB |||||  
QY 2132 CAGAACTTACAGATTATGACATAGATCAAGCGGCAATCTTGTGGAATGATTTCTTGAAG 2191  
DB |||||  
QY 2412 AACAAATCTCAGGAAAAAATAATGTTATGGATGAATAAATACTGGCAAAACAACCTTA 2471  
DB |||||  
QY 2192 AATTATATCAAAAGAAAAAATGCTGTTATTAGATGAAGTTAAAAATGCCAAACAACCTTA 2251  
DB |||||  
QY 2472 GTGAGTCTGTAATCTTACTCCAAATGGAGACTTT-----TCTGGGAATGATGGACAT 2525  
DB |||||  
QY 2252 GTCAATCTCGAAATGTACTTCAAAACGGGGAATTTGAAATCGGCTACGCTTTGGTGGACAA 2311  
DB |||||  
QY 2526 TCGGTAATGATATTATCATAGGATCCAATAATCCTATTATTTAAAGGAAAAATTTCTACAGA 2585  
DB |||||  
QY 2312 CAAGTGATATATACAAATTCAGAGATGATCTTATTTTAAAGGGCATTACCTTCATA 2371  
DB |||||  
QY 2586 TGGGTGAGCAGCAGACATATATGGAACCTTATTTCCAACTTATATCTGTCAAAAAATAG 2645  
DB |||||  
QY 2372 TGTCTGGGGCGAGAAATTTGATGGTACGATATTTCCGACCTATATATTCCAAAAAATTC 2431  
DB |||||  
QY 2646 ATGAGTCTAAATTAACCAATATACAGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGTA 2705  
DB |||||  
QY 2432 ATGAATCAAAATTAACCAATATACAGTTATCGAGTAAGGGGAATTTGTAGGAAGTAGTA 2491  
DB |||||  
QY 2706 AAGATTGAAATTAATGGTAACAGTTTACGGGAAAGAAATTTGATGCTATCATCAATGTTTC 2765  
DB |||||  
QY 2492 AAGATGTAGAACTAGTGTGTTTACGGCTATGGGGAAGAAATTTGATGCCATGAAATGTTTC 2551  
DB |||||  
QY 2766 CAAATGATTTGGCCTATATGACAGCCTTAATCCTTTATGTTGGAGATTCGCTGTGAATCAT 2825  
DB |||||  
QY 2552 CAGCTGATTTAAACTATCTGTATCTCTTAC-----CTTTGATTTGTGAAGGT 2599  
DB |||||  
QY 2826 CGTCTCAGTATGTGAGCCAGGGTATCTTACCAACACAGATGGATATGCTCCCGATATGT 2885  
DB |||||  
QY 2600 CTAATCGTTGTGAGCGTCCCGCTGTGCGCGGTAAACATTTGGGAACACCTTCTGATATGTCGT 2659  
DB |||||

Search completed: December 19, 2005, 14:37:48  
Job time : 2221.9 secs

QY 2886 ATGATGCGCCGAAAAATATAGATAGAAAGCATGTGAAGTGTACAGTCGTCAATCCATTTG 2945  
DB |||||  
QY 2660 ATTCTATGCCAATATGATATACAGGAAAAAGCATGTCTGATGTCTAGGATTCCTCAATTTA 2719  
DB |||||  
QY 2946 ATTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGATAGTATGATGTTCTTAT 3005  
DB |||||  
QY 2720 GTTTCACTATTGATACAGGGGCATTAGATACAAATGAAATAATAGGGTTGGTCTATGT 2779  
DB |||||  
QY 3006 TAAAAATTTCTAATCCAGATGGATAGCTACAGTAGGGATCTAGAGTCAATTTGAAGAAG 3065  
DB |||||  
QY 2780 TTAATAATATCTCTCCAGATGGATACGCATCATTTAGATTAATTTAGAGTAAATTTGAAGAAG 2839  
DB |||||  
QY 3066 GACCACTAACAGGTGAAGCATTTGGCAGATGTGAAACAAAGAAAGAAAGAAATGAAACCAAC 3125  
DB |||||  
QY 2840 GGCCATAGATGGGGAAGCACTGTACGGGTGAAACACATGGAGAGAAATGAAACGATC 2899  
DB |||||  
QY 3126 ACATGAGAAAAAAGCTTTGGGAAACACAAAGCCCTATGATCCAGCAAAACAGGCTGTAG 3185  
DB |||||  
QY 2900 AAATGGAAGCAAAACGTTGGGAAACACAAAGCATATGATGTAGCGAAACAAGCCATTA 2959  
DB |||||  
QY 3186 ATGCATTTATTACAAATGAAACAGA-----GTTACACTATCATATTTACTTTAGATCATTA 3239  
DB |||||  
QY 2960 ATGCTTTATTTCAAATATGTACAAGATGAGGCTTTACAGTTTGTATACGACACTCGCTCAA 3019  
DB |||||  
QY 3240 TTCAAAACGCTGATCGACTGCTACAGTCGATTCCTTATGTATACCATTAATTTGTTTACCGA 3299  
DB |||||  
QY 3020 TTCAGTACGCTGATTTTGGTACATTCATTCATATGTTACATATGTTGTTGTCTAG 3079  
DB |||||  
QY 3300 ATGCTCCAGGTATGAATATGATATATCAAGAGTTAAACGACGCTATCATCAAGGTT 3359  
DB |||||  
QY 3080 ATGCTCCAGGTATGAATATGATCATCTATGTAGTGGATGACGAGTGGCAACAGCGC 3139  
DB |||||  
QY 3360 ATAAATTTATGATGACGAAATGTCATAACAAATGCTGACCTTTACACAAGGATTTACAGG 3419  
DB |||||  
QY 3140 GTTATTTGTTATGATACAAAGAAATATTTATTAATAATGTTGATTTTACACAAGGGTAAATGG 3199  
DB |||||  
QY 3420 GATGGCAGCAACAGGAAATGCCGCGTACACAAATGATGAGCTTCAAGATCATCATGATGTTTC 3479  
DB |||||  
QY 3200 GGTGGCATGTAACTGGAAATGACAGTACAAACAAATAGATGTTGTTCTGTTATGTTTC 3259  
DB |||||  
QY 3480 TATCAAAATGGAGCGCGGGGTATCTCAAACTTGCATCTCAAGATCATCATGATGATG 3539  
DB |||||  
QY 3260 TATCTAATTTGGAGTGTGCGGTATCTCAAAATGTCATCTCCAAACATAATCATGGGTATG 3319  
DB |||||  
QY 3540 TGTAGCTGTGATTTGCCAAAAAGAGGACCTGGAAAAAGGGTATGTAAACGATGATGAT 3599  
DB |||||  
QY 3320 TCTTACGTGTTATTTGCCAAAAAGAGGACCTGGAAATGGGTATGTCAACGCTTATGGAT 3379  
DB |||||  
QY 3600 GTAATGGAAGCAGGAAACACCTTAAGTTCACCTTTTGGCAAGAGGATATATGACAAAAA 3659  
DB |||||  
QY 3380 GTGAGAGATCAAGAAAAATTTGACGTTTACGTTCTTGTGAGAGAGATATATTTACGAGA 3439  
DB |||||  
QY 3660 CAGTAGAGGTAATTTCCAGAAAGTGTGTTGATCGGATTCGAAATGAGAGAACCGAAGGTA 3719  
DB |||||  
QY 3440 CAGTAGATGTTATTTCCAGATACAGATCGTGTACGAATTTGAGATAGGCGAAACCGAAGGTT 3499  
DB |||||  
QY 3720 CATTTTATATAGATGATGATGCTGCTTTGTTGATGCAAG 3758  
DB |||||  
QY 3500 CGTTTTATATCGAAAGCATTTGAATTAATTTTGCATGAACG 3538  
DB |||||

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:48:03 ; Search time 2957.36 Seconds  
(without alignments)  
16721.276 Million cell updates/sec

Title: US-10-781-979-1

Perfect score: 5980

Sequence: 1 tacatgaataacataaagag.....ttctaaaaagcctctgtat 5980

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA\_Main:\*

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2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

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7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 5980  | 100.0       | 5980   | 8     | US-10-781-979-1   |
| 2          | 2082  | 34.8        | 2082   | 8     | US-10-781-979-2   |
| 3          | 2073  | 34.7        | 2073   | 8     | US-10-781-979-4   |
| 4          | 1686  | 28.2        | 1686   | 8     | US-10-781-979-6   |
| 5          | 967   | 16.2        | 4391   | 9     | US-10-929-754-4   |
| 6          | 855   | 14.3        | 2145   | 8     | US-10-782-141-1   |
| 7          | 789   | 13.2        | 3684   | 9     | US-10-929-754-2   |
| 8          | 747   | 12.5        | 2019   | 8     | US-10-782-141-2   |
| 9          | 739.8 | 12.4        | 2010   | 8     | US-10-782-141-4   |
| 10         | 390   | 6.5         | 4359   | 5     | US-10-120-544A-3  |
| 11         | 390   | 6.5         | 4359   | 10    | US-11-091-654-3   |
| 12         | 380.8 | 6.4         | 3504   | 5     | US-10-089-678-2   |
| 13         | 380.8 | 6.4         | 3690   | 5     | US-10-089-678-3   |
| 14         | 318.6 | 5.3         | 4366   | 5     | US-10-120-544A-19 |
| 15         | 318.6 | 5.3         | 4366   | 10    | US-11-091-654-19  |
| 16         | 313   | 5.2         | 4896   | 6     | US-09-756-526A-3  |
| 17         | 313   | 5.2         | 4896   | 6     | US-10-345-020-3   |
| 18         | 313   | 5.2         | 4896   | 6     | US-10-342-821-3   |
| 19         | 312.2 | 5.2         | 4359   | 5     | US-10-120-544A-17 |
| 20         | 312.2 | 5.2         | 4359   | 10    | US-11-091-654-17  |
| 21         | 310.4 | 5.2         | 6930   | 3     | US-09-756-526A-1  |
| 22         | 310.4 | 5.2         | 6930   | 6     | US-10-345-020-1   |
| 23         | 310.4 | 5.2         | 6930   | 6     | US-10-342-821-1   |

|    |       |     |      |    |                  |                    |
|----|-------|-----|------|----|------------------|--------------------|
| 24 | 308.2 | 5.2 | 4188 | 5  | US-10-120-544A-5 | Sequence 5, Appli  |
| 25 | 308.2 | 5.2 | 4188 | 10 | US-11-091-654-5  | Sequence 5, Appli  |
| 26 | 307   | 5.1 | 3621 | 5  | US-10-032-717-1  | Sequence 1, Appli  |
| 27 | 307   | 5.1 | 3621 | 6  | US-10-414-637-1  | Sequence 1, Appli  |
| 28 | 307   | 5.1 | 3621 | 7  | US-10-606-320-1  | Sequence 1, Appli  |
| 29 | 307   | 5.1 | 3621 | 8  | US-10-746-914-1  | Sequence 1, Appli  |
| 30 | 307   | 5.1 | 3621 | 10 | US-11-021-115-5  | Sequence 5, Appli  |
| 31 | 307   | 5.1 | 3633 | 5  | US-10-032-717-3  | Sequence 3, Appli  |
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| 34 | 307   | 5.1 | 3633 | 8  | US-10-746-914-3  | Sequence 3, Appli  |
| 35 | 307   | 5.1 | 4874 | 5  | US-10-032-717-27 | Sequence 27, Appli |
| 36 | 307   | 5.1 | 4874 | 6  | US-10-414-637-27 | Sequence 27, Appli |
| 37 | 307   | 5.1 | 4874 | 7  | US-10-606-320-17 | Sequence 17, Appli |
| 38 | 307   | 5.1 | 4874 | 8  | US-10-746-914-17 | Sequence 17, Appli |
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| 41 | 307   | 5.1 | 6613 | 7  | US-10-606-320-18 | Sequence 18, Appli |
| 42 | 307   | 5.1 | 6613 | 8  | US-10-746-914-18 | Sequence 18, Appli |
| 43 | 279.2 | 4.7 | 3507 | 7  | US-10-614-524-3  | Sequence 3, Appli  |
| 44 | 278   | 4.6 | 3465 | 10 | US-11-018-615-26 | Sequence 26, Appli |
| 45 | 275.6 | 4.6 | 3471 | 5  | US-10-099-285-71 | Sequence 71, Appli |

ALIGNMENTS

RESULT 1

US-10-781-979-1

; Sequence 1, Application US/10781979

; Publication No. US20040250311A1

; GENERAL INFORMATION:

; APPLICANT: Carozzi, Nadine

; APPLICANT: Hargiss, Tracy

; APPLICANT: Kozielec, Michael G.

; APPLICANT: Carr, Nicholas B.

; APPLICANT: Carr, Brian

; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and Methods for Its Use

; FILE REFERENCE: 045600/274147

; CURRENT APPLICATION NUMBER: US/10/781,979

; PRIOR FILING DATE: 2004-02-20

; PRIOR APPLICATION NUMBER: 60/448,797

; PRIOR FILING DATE: 2003-02-20

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 5980

; TYPE: DNA

; ORGANISM: Bacillus thuringiensis

US-10-781-979-1

|                       |                 |   |           |              |  |
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| Best Local Similarity | 100.0%;         | Pred. No. 0;  |           |              |  |
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| Db                    | 1               | TACATGCAATACATAAAGAGAGGTTTAAATAATCAATACCTCACCACCAAAATATCGGTT  | 60        |              |  |
| QY                    | 61              | TATTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATATATAGAAAGACAC | 120       |              |  |
| Db                    | 61              | TATTTGTAGAAACATTTGTACAGGAATACATTTGGGGTACTACGAATATATAGAAAGACAC | 120       |              |  |
| QY                    | 121             | CTAACATATATTTATTAGTGCTTTAAAAATAGGACTATATAAGAGTGAAGGATGA       | 180       |              |  |
| Db                    | 121             | CTAACATATATTTATTAGTGCTTTAAAAATAGGACTATATAAGAGTGAAGGATGA       | 180       |              |  |
| QY                    | 181             | GTCCATATCAATAAATAAATGAATATGAATTCGAATCCTCATCGAATACACAAATA      | 240       |              |  |
| Db                    | 181             | GTCCATATCAATAAATAAATGAATATGAATTCGAATCCTCATCGAATACACAAATA      | 240       |              |  |
| QY                    | 241             | CGCCAAACAGATATCTCTTTTGCAAAATAATCGGATATGTCTACTATGTCTTGAATGATT  | 300       |              |  |

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Db  
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Db  
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Db  
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QY 3781 GCACACGGGTAAATATGATGAGCAAAAGTTTATTAATGAAAATTAATCAAAATTAAGCTAGCGA 3840  
DB |||||  
QY 3781 GCACACGGGTAAATATGATGAGCAAAAGTTTATTAATGAAAATTAATCAAAATTAAGCTAGCGA 3840  
DB |||||  
QY 3841 TGTGTATTACCAAGGGTATACAAACAACTATTAACCAAGACTCTAGTAATATGTAATCA 3900  
DB |||||  
QY 3841 TGTGTATTACCAAGGGTATACAAACAACTATTAACCAAGACTCTAGTAATATGTAATCA 3900  
DB |||||  
QY 3901 AAATTAATCTAACAATGATGACCTGCATTCGCGTTGCACATGTAACCAAGGGCATTAATC 3960  
DB |||||  
QY 3901 AAATTAATCTAACAATGATGACCTGCATTCGCGTTGCACATGTAACCAAGGGCATTAATC 3960  
DB |||||  
QY 3961 TGGCTGTACATGTAATCAAGGATATAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020  
DB |||||  
QY 3961 TGGCTGTACATGTAATCAAGGATATAACCGTTTAAACGATTTCTAAATTAAGAAATCAACATCAT 4020  
DB |||||  
QY 4021 TGGGAAAAATTAACAACTACTCACAATACTTATTCGATATCATTAACATTAAGCTTTACAAA 4080  
DB |||||  
QY 4021 TGGGAAAAATTAACAACTACTCACAATACTTATTCGATATCATTAACATTAAGCTTTACAAA 4080  
DB |||||  
QY 4081 TAAACGACATATTTCTAGAAGAGTCTCTTAAATCTTAAATTAAGGAGATTTTTCGTTT 4140  
DB |||||  
QY 4081 TAAACGACATATTTCTAGAAGAGTCTCTTAAATCTTAAATTAAGGAGATTTTTCGTTT 4140  
DB |||||  
QY 4141 CCCCATAATTTGATTAATGAAAATATCTCTTTTACAGAAAGATTTTAGCTGATTTGTTT 4200  
DB |||||  
QY 4141 CCCCATAATTTGATTAATGAAAATATCTCTTTTACAGAAAGATTTTAGCTGATTTGTTT 4200  
DB |||||  
QY 4201 GTGCAAGCAGCAATTCCTGAAAAATGCAAAAAAATTCAGAGGCAATGCAAGCTATTTT 4260  
DB |||||  
QY 4201 GTGCAAGCAGCAATTCCTGAAAAATGCAAAAAAATTCAGAGGCAATGCAAGCTATTTT 4260  
DB |||||  
QY 4261 TAAATGTTAAATTTTGGTATTTCCAGAAAGATAAGCAATTTTCGTAACGATAACCTTTT 4320  
DB |||||  
QY 4261 TAAATGTTAAATTTTGGTATTTCCAGAAAGATAAGCAATTTTCGTAACGATAACCTTTT 4320  
DB |||||  
QY 4321 GTGAATGCAATGATATGAGCATGAGCAACAAACGCTCCACCAATGCAAGGTAAAGCCGG 4380  
DB |||||  
QY 4321 GTGAATGCAATGATATGAGCATGAGCAACAAACGCTCCACCAATGCAAGGTAAAGCCGG 4380  
DB |||||  
QY 4381 TTATCAACCAATATATAGGATTCATTCAGCAACCAATTTCTAAGTTTGAAGTAACTATGACACT 4440  
DB |||||  
QY 4381 TTATCAACCAATATATAGGATTCATTCAGCAACCAATTTCTAAGTTTGAAGTAACTATGACACT 4440  
DB |||||  
QY 4441 TTTTGTTCGTAAACAGTCGGCAATTAATGAAAATAGGAGCTCCGCTCTTTCGTTTGAAT 4500  
DB |||||  
QY 4441 TTTTGTTCGTAAACAGTCGGCAATTAATGAAAATAGGAGCTCCGCTCTTTCGTTTGAAT 4500  
DB |||||  
QY 4501 GGTACATAACCTTAGTTTCACTTAAATTAATAATCAAGGCTTCAATTTGCTTTCTTGATG 4560  
DB |||||  
QY 4501 GGTACATAACCTTAGTTTCACTTAAATTAATAATCAAGGCTTCAATTTGCTTTCTTGATG 4560  
DB |||||  
QY 4561 CGGGTTAAATTCCTTGTGTTTAAAGCTTCTTAAATAGACCTTCTAATCTGCTACTCGG 4620  
DB |||||  
QY 4561 CGGGTTAAATTCCTTGTGTTTAAAGCTTCTTAAATAGACCTTCTAATCTGCTACTCGG 4620  
DB |||||  
QY 4621 AAAAACTTCACTTGATATCCCTGTTTCAACAGCTTCAACACCTTAATGCTGTAGCTAATGT 4680  
DB |||||

Db 4621 AAAAACTTCACCTGATCCCTGTTTACAGCCCTTCAAACTTAATGCTAGCTAAATGT 4680  
QY GTTTTCCAGTTCACGAGATCAAGTAATAAAGATTTTGTTCCTTCAAAAAATCG 4740  
Db GTTTTCCAGTTCACGAGATCAAGTAATAAAGATTTTGTTCCTTCAAAAAATCG 4740  
QY AATTCAAAATGTTTCTTGATTCGTTGTAGATGGCAGATGAATTTGTTCACTCCATTCA 4800  
Db AATTCAAAATGTTTCTTGATTCGTTGTAGATGGCAGATGAATTTGTTCACTCCATTCA 4800  
QY TAATTTCTGAGCCATTTAACTCTCGAAATTTTCGCTTCTTGATTAAGTTTCTGCTATTTT 4860  
Db TAATTTCTGAGCCATTTAACTCTCGAAATTTTCGCTTCTTGATTAAGTTTCTGCTATTTT 4860  
QY TTGTTTGTGACGAGATCAATCTCTATATTGAATAATACAGCAGAAATTTGTTCTTTGGTT 4920  
Db TTGTTTGTGACGAGATCAATCTCTATATTGAATAATACAGCAGAAATTTGTTCTTTGGTT 4920  
QY TCAAAAGGATTTTCATCAATAATGGTCTATAATAATAGCTTAAATGCAAGTATTTACAGCG 4980  
Db TCAAAAGGATTTTCATCAATAATGGTCTATAATAATAGCTTAAATGCAAGTATTTACAGCG 4980  
QY TCTTGACGTTTTCGTTGTATCAATAAGATGAACCCCTTTCTTAAAGTTGGCAAGCT 5040  
Db TCTTGACGTTTTCGTTGTATCAATAAGATGAACCCCTTTCTTAAAGTTGGCAAGCT 5040  
QY TTGATCATATTCTGAAAGATCTGTTTCGTAATCTATTAATAACAGGTGGCTATGGTTT 5100  
Db TTGATCATATTCTGAAAGATCTGTTTCGTAATCTATTAATAACAGGTGGCTATGGTTT 5100  
QY CTTGCAATTTTGTGATAGTCACTGTTTGTAGTCTGCAATATGATATCGAGTTCGTAG 5160  
Db CTTGCAATTTTGTGATAGTCACTGTTTGTAGTCTGCAATATGATATCGAGTTCGTAG 5160  
QY GAGCTTTTTCACCAATCTTCAATCTCTAACAGTAAGTGTAGTCTGCTGTATGATATT 5220  
Db GAGCTTTTTCACCAATCTTCAATCTCTAACAGTAAGTGTAGTCTGCTGTATGATATT 5220  
QY TTTGAATTAATAATTGAATTCCTGTTTAAACAAGCTTTTCTTTCATCCTTATGAAGAGCA 5280  
Db TTTGAATTAATAATTGAATTCCTGTTTAAACAAGCTTTTCTTTCATCCTTATGAAGAGCA 5280  
QY GATAATCTTGAAACCCGCTGAGGTAATAATTTGAAAAATCTAGAAATACGAAACCGGTG 5340  
Db GATAATCTTGAAACCCGCTGAGGTAATAATTTGAAAAATCTAGAAATACGAAACCGGTG 5340  
QY GTTTCTTTTCCCAATCTTCAAAAATCTCTTCCCATAGATCGGCTACTCGTGTGCATAT 5400  
Db GTTTCTTTTCCCAATCTTCAAAAATCTCTTCCCATAGATCGGCTACTCGTGTGCATAT 5400  
QY ACGGTCTGATTTCTGTAATAATGTTCTCGCTTCTCGGGTATACATGTAATTTGATCCC 5460  
Db ACGGTCTGATTTCTGTAATAATGTTCTCGCTTCTCGGGTATACATGTAATTTGATCCC 5460  
QY ATTCTTTTAAATGATAATCACTGTTTAAAGTAAACAAAACGTTCTTGATCCACTGTG 5520  
Db ATTCTTTTAAATGATAATCACTGTTTAAAGTAAACAAAACGTTCTTGATCCACTGTG 5520  
QY ATTCTTCCATATTTATTTACCGTTGTTGTGTCATTTGAGAAAGCCGTTAGGCTTCCAAA 5580  
Db ATTCTTCCATATTTATTTACCGTTGTTGTGTCATTTGAGAAAGCCGTTAGGCTTCCAAA 5580  
QY GGTAAATGGTTTCAATGCAGCTTTATCATCTATCCAAAGGCTTCTCAATCATGACTTCTTC 5640  
Db GGTAAATGGTTTCAATGCAGCTTTATCATCTATCCAAAGGCTTCTCAATCATGACTTCTTC 5640  
QY TCAATAATGAGGCTTTCTGATCTTCTATTTGCTTGTACTTCTAAACATTTGTGGAGTTGA 5700  
Db TCAATAATGAGGCTTTCTGATCTTCTATTTGCTTGTACTTCTAAACATTTGTGGAGTTGA 5700  
QY GAAAAACTCTCCATAATCGAGCGGTTGTAAACCAATTTGTTCTGTGTATAACTGACTTTC 5760  
Db GAAAAACTCTCCATAATCGAGCGGTTGTAAACCAATTTGTTCTGTGTATAACTGACTTTC 5760

Db 5701 GAAAAACTCTCCATAATCGAGCGGTTGTAAACCAATTTGTTCTGTGTATAACTGACTTTC 5760  
QY CGTTCAACGTTTCCCTCTTTTCATGCCCCGTATAAGGATTACAAGGTTTGCACTTTCAAAGTTA 5820  
Db CGTTCAACGTTTCCCTCTTTTCATGCCCCGTATAAGGATTACAAGGTTTGCACTTTCAAAGTTA 5820  
QY TAATGCATTTGAAATTTGAAAAATGCAATCGATCCGATTAAGTTCGATTATCACCTTTCTCTACT 5880  
Db TAATGCATTTGAAATTTGAAAAATGCAATCGATCCGATTAAGTTCGATTATCACCTTTCTCTACT 5880  
QY 5881 GTGACTACAGCGGAGATGAAGTTATCAATTCGAAGATCGGTTGGTACACCACGCTTGA 5940  
Db 5881 GTGACTACAGCGGAGATGAAGTTATCAATTCGAAGATCGGTTGGTACACCACGCTTGA 5940  
QY 5941 TGAATAATCGTTTAAAGCCTTCTAAAAAGCCTTCTGTAT 5980  
Db 5941 TGAATAATCGTTTAAAGCCTTCTAAAAAGCCTTCTGTAT 5980  
  
RESULT 2  
US-10-781-979-2  
; Sequence 2, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Harliss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
; FILE REFERENCE: Methods for Its Use  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,797  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 2082  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2082)  
US-10-781-979-2  
  
Query Match 34.8%; Score 2082; DB 8; Length 2082;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 168 GTGAAAAAGATGAGTCCATATCAAAATAAAAATGAATATGAAATATGGAATCTCTCATCG 227  
Db 1 GTGAAAAAGATGAGTCCATATCAAAATAAAAATGAATATGAAATATGGAATCTCTCATCG 60  
  
QY 228 AATAACACAATAACGCCAAACAGATATCCTTTTGCATAATAATCGGGATATGCTACTATG 287  
Db 61 AATAACACAATAACGCCAAACAGATATCCTTTTGCATAATAATCGGGATATGCTACTATG 120  
  
QY 288 TCTTGGAAATGATTGTTCAGGGAATCTCATGGGAATGAAATTTGGGAATCAGTCGAAACGATA 347  
Db 121 TCTTGGAAATGATTGTTCAGGGAATCTCATGGGAATGAAATTTGGGAATCAGTCGAAACGATA 180  
  
QY 348 ACAAGTATTTGGGATAAAATCTTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 407  
Db 181 ACAAGTATTTGGGATAAAATCTTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240  
  
QY 408 ACATATTATTAATAATAGGAAAACTAATTCGACATAATTCGTCAAACTGTGTGACGACTT 467  
Db 241 ACATATTATTAATAATAGGAAAACTAATTCGACATAATTCGTCAAACTGTGTGACGACTT 300  
  
QY 468 TCTATATGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 527  
Db TCTATATGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 527



Db 301 TCTATATGTGATTTATTATCTATTAATTCTGTAAGAGGTAGCCGATAGTGTGTTTAAAGTAT 360  
Qy 528 GCGATTTGAGATTTTTCGCGTAAATTTGAAAAATTTATAGAGAGTATTATCTTCTTATCTT 587  
Db 361 GCGATTTGAGATTTTTCGCGTAAATTTGAAAAATTTATAGAGAGTATTATCTTCTTATCTT 420  
Qy 588 GGGCTTTGGCTTAAAGACGGTAAACCACTTCAAAAAGACAAATAAATCTTGATATCGGACAA 647  
Db 421 GGGCTTTGGCTTAAAGACGGTAAACCACTTCAAAAAGACAAATAAATCTTGATATCGGACAA 480  
Qy 648 TTAGTTTATTTTAAATTTTCAAGATTTTCAAGAGATTTCAATGAAATTTAGAGGGTCAATTG 707  
Db 481 TTAGTTTATTTTAAATTTTCAAGATTTTCAAGAGATTTCAATGAAATTTAGAGGGTCAATTG 540  
Qy 708 TCAAGAAACAATGCTCAAGTATGTTTATCTACTACTTTTGCACAAAGCTGCAAAATGTGCAG 767  
Db 541 TCAAGAAACAATGCTCAAGTATGTTTATCTACTACTTTTGCACAAAGCTGCAAAATGTGCAG 600  
Qy 768 TTATTAATTAAGGGATGCAAGTTCAATATAAAGACAAATGGTTCCCAATTTTGGAGTGCA 827  
Db 601 TTATTAATTAAGGGATGCAAGTTCAATATAAAGACAAATGGTTCCCAATTTTGGAGTGCA 660  
Qy 828 GAGAAATGTAAGATCGGAATTAATATACCTTAAACAGTGGTGTGATTTTACCGGTGATTAC 887  
Db 661 GAGAAATGTAAGATCGGAATTAATATACCTTAAACAGTGGTGTGATTTTACCGGTGATTAC 720  
Qy 888 TATGAGCGATTTAAATGCAAAACGGCAGAGATATACCAATATTGTTTATATTGTTATCAG 947  
Db 721 TATGAGCGATTTAAATGCAAAACGGCAGAGATATACCAATATTGTTTATATTGTTATCAG 780  
Qy 948 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 1007  
Db 781 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 840  
Qy 1008 AAATTTCTAGAGAAATGAGTTGGCGGTATTTGATATATCGCTATATTTCCAACTTAT 1067  
Db 841 AAATTTCTAGAGAAATGAGTTGGCGGTATTTGATATATTTGATATATTTCCAACTTAT 900  
Qy 1068 GATTTTCAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT 1127  
Db 901 GATTTTCAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT 960  
Qy 1128 GCAGTGGGATTTTCAATCGGAACTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 1187  
Db 961 GCAGTGGGATTTTCAATCGGAACTTATAGTTGGTTACGGAATTTGGCCTAATCTTTAAT 1020  
Qy 1188 GGGTTAGAGCTTAATGGAACACGGGACCTGGTTTATGTTACTGGCTTAGCAAAATAGGT 1247  
Db 1021 GGGTTAGAGCTTAATGGAACACGGGACCTGGTTTATGTTACTGGCTTAGCAAAATAGGT 1080  
Qy 1248 ATATATAATCAGTATGTTTCGAGATATTTTCCGCGTGGGTAGGAACCTCGCTATTATGAA 1307  
Db 1081 ATATATAATCAGTATGTTTCGAGATATTTTCCGCGTGGGTAGGAACCTCGCTATTATGAA 1140  
Qy 1308 GACTACACAAAGGGTAAACGGTATTTTTCACAGTATGTTCTGGAACCTACGAGTAATGATCTA 1367  
Db 1141 GACTACACAAAGGGTAAACGGTATTTTTCACAGTATGTTCTGGAACCTACGAGTAATGATCTA 1200  
Qy 1368 CGTAATATGATTTTCAAGATGCGGATGATATAAATAATCTTCAATAGCTATCATGAAC 1427  
Db 1201 CGTAATATGATTTTCAAGATGCGGATGATATAAATAATCTTCAATAGCTATCATGAAC 1260  
Qy 1428 CTAGTAGGAGACTACCGCTAGACAGAGATCGTGTTCGAGGAGATTTTCGTTAGG 1487  
Db 1261 CTAGTAGGAGACTACCGCTAGACAGAGATCGTGTTCGAGGAGATTTTCGTTAGG 1320  
Qy 1488 GTAGGGGGACCTGATTTTAAATTTATGATGTCAGGTAAATAGGGCTTAACGAGATGACAAAT 1547  
Db 1321 GTAGGGGGACCTGATTTTAAATTTATGATGTCAGGTAAATAGGGCTTAACGAGATGACAAAT 1380  
Qy 1548 GAATCTACGTTCCCACTGTATTGCACTCTAAATGGTGTAGAGACCTCTCATAGATTA 1607  
Db 1381 GAATCTACGTTCCCACTGTATTGCACTCTAAATGGTGTAGAGACCTCTCATAGATTA 1440

Qy 1608 TCAAAATCGCGCATGTGTTGTATATGGAACCTCCAGAGTTAACTGATATATGTTGGACACAT 1667  
Db 1441 TCAAAATCGCGCATGTGTTGTATATGGAACCTCCAGAGTTAACTGATATATGTTGGACACAT 1500  
Qy 1668 ACAAGTTTAAACCGTGAATAATAATTAAGAACCAATCAAAATTAACAATAACCCGCGGTG 1727  
Db 1501 ACAAGTTTAAACCGTGAATAATAATTAAGAACCAATCAAAATTAACAATAACCCGCGGTG 1560  
Qy 1728 AAGAGTTATTACCTTCAAAATTTATCTGCTAAATGCTTATATGCTTATATCTATGTAATAAAGGCACT 1787  
Db 1561 AAGAGTTATTACCTTCAAAATTTATCTGCTAAATGCTTATATGCTTATATCTATGTAATAAAGGCACT 1620  
Qy 1788 CATACAGTGGGATTTAATCCGTTTAAAGAACCAAAATCAGAGTATAACGCAAGTTTAT 1847  
Db 1621 CATACAGTGGGATTTAATCCGTTTAAAGAACCAAAATCAGAGTATAACGCAAGTTTAT 1680  
Qy 1848 GCAGGTGGCGAAATTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTATT 1907  
Db 1681 GCAGGTGGCGAAATTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTATT 1740  
Qy 1908 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTAGTGTATATCTTTATCCAGGAGGT 1967  
Db 1741 CGTTTTCGTTATGCTGCAGATAAAGCTGCTTCTTTAGTGTATATCTTTATCCAGGAGGT 1800  
Qy 1968 TGGGGTTCAAAATCGTTTGTATCGCTTGAAGAAATCTTACTCTGGAATTTATGAGATTTA 2027  
Db 1801 TGGGGTTCAAAATCGTTTGTATCGCTTGAAGAAATCTTACTCTGGAATTTATGAGATTTA 1860  
Qy 2028 AAATATAGTGAATTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAACATT 2087  
Db 1861 AAATATAGTGAATTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAACATT 1920  
Qy 2088 CAGATGATGTGAGATGCAAGCGAATAGTTTTCATCAGATGATAACGTGGTTCTCGAC 2147  
Db 1921 CAGATGATGTGAGATGCAAGCGAATAGTTTTCATCAGATGATAACGTGGTTCTCGAC 1980  
Qy 2148 AAAATTTGAATTCCTCCCAAGTAATACAACTTTTGAATATGAGGAGAACCGGACCTA 2207  
Db 1981 AAAATTTGAATTCCTCCCAAGTAATACAACTTTTGAATATGAGGAGAACCGGACCTA 2040  
Qy 2208 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTA 2249  
Db 2041 GAAAAACAAAGAACCGGTGAACGATCTGTTTACCAATTA 2082

RESULT 3  
US-10-781-979-4  
; Sequence 4, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCES: 045600/274147  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,797  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2073  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2073)  
US-10-781-979-4

| Query Match   |      |  |      | 34.7%; Score 2073; DB 8; Length 2073; |      |  |      |
|---|------|--|------|---------------------------------------|------|--|------|
| Best Local Similarity   |      |  |      | 100.0%; Pred. No. 0;                  |      |  |      |
| Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |      |  |      |                                       |      |  |      |
| Qy  | 177  | ATGAGTCCATATCAAAATATAAATGAATATGAAATATTTGGAATCCTCATCGAATAACACA  | 236  | Qy                                    | 1197 | GCTAATGGAAACACGGGACCTGGTTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT     | 1256 |
| Db  | 1    | ATGAGTCCATATCAAAATATAAATGAATATGAAATATTTGGAATCCTCATCGAATAACACA  | 60   | Db                                    | 1021 | GCTAATGGAAACACGGGACCTGGTTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT     | 1080 |
| Qy  | 237  | AATACGCCAAACAGATATCTTTTGCAAAATAATCGGGATATGCTACTATGCTTCGGAAT    | 296  | Qy                                    | 1257 | GAGTATGTTTCGAGATATTTTCCCGCTGGGTAGGAACTCGTCATTATAGAAGACTACACA     | 1316 |
| Db  | 61   | AATACGCCAAACAGATATCTTTTGCAAAATAATCGGGATATGCTACTATGCTTCGGAAT    | 120  | Db                                    | 1081 | GAGTATGTTTCGAGATATTTTCCCGCTGGGTAGGAACTCGTCATTATAGAAGACTACACA     | 1140 |
| Qy  | 297  | GATTTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT   | 356  | Qy                                    | 1317 | AAGGGTAAACGGTATTTTTCAACGTATGCTCTGGAACTACGAGTAATGATCTACGTAATATT   | 1376 |
| Db  | 121  | GATTTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATAACAAGTATT   | 180  | Db                                    | 1141 | AAGGGTAAACGGTATTTTTCAAGGTATGCTCTGGAACTACGAGTAATGATCTACGTAATATT   | 1200 |
| Qy  | 357  | GGGATAAATCTTATAGAGTTTCGTAGATAGAACTAGTTTGGGTGGAATTAATACACTATTA  | 416  | Qy                                    | 1377 | GATTTTCAGATGCGGATGTATATAAAATTAATTTCACTTAGCTATCATGAACCTAGTAGGA    | 1436 |
| Db  | 181  | GGGATAAATCTTATAGAGTTTCGTAGATAGAACTAGTTTGGGTGGAATTAATACACTATTA  | 240  | Db                                    | 1201 | GATTTTCAGATGCGGATGTATATAAAATTAATTTCACTTAGCTATCATGAACCTAGTAGGA    | 1260 |
| Qy  | 417  | TCAATAATAGGAAACCTAATTCGACTAATCGTCAAACTGTGTGACACCTTTCTATATGT    | 476  | Qy                                    | 1437 | GAGACTACCGCTAGACACAGAGTATCGTGTTCCTCAAGGCGAGATTTTTCGTAGGGTAGGGGA  | 1496 |
| Db  | 241  | TCAATAATAGGAAACCTAATTCGACTAATCGTCAAACTGTGTGACACCTTTCTATATGT    | 300  | Db                                    | 1261 | GAGACTACCGCTAGACACAGAGTATCGTGTTCCTCAAGGCGAGATTTTTCGTAGGGTAGGGGA  | 1320 |
| Qy  | 477  | GATTTTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAAGTGATGCGATTGCA    | 536  | Qy                                    | 1497 | CCTGATTTAAATATATGATGCGAGTAAATAATGGGCTAAGCAGGATGACAAATGGAATCTACG  | 1556 |
| Db  | 301  | GATTTTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAAGTGATGCGATTGCA    | 360  | Db                                    | 1321 | CCTGATTTAAATATATGATGCGAGTAAATAATGGGCTAAGCAGGATGACAAATGGAATCTACG  | 1380 |
| Qy  | 537  | GATTTTGACGGTAAATTGAAATTTATAGAGATATTAATCTTTCTTATCTTTGGGGCTTGG   | 596  | Qy                                    | 1557 | TTCCCACTTTGATTTGCGACTCTAATGGTGTAGAGGACCTCTCATAGATATCAAAATGCG     | 1616 |
| Db  | 361  | GATTTTGACGGTAAATTGAAATTTATAGAGATATTAATCTTTCTTATCTTTGGGGCTTGG   | 420  | Db                                    | 1381 | TTCCCACTTTGATTTGCGACTCTAATGGTGTAGAGGACCTCTCATAGATATCAAAATGCG     | 1440 |
| Qy  | 597  | CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGGACAAATTAGTTTAT   | 656  | Qy                                    | 1617 | GCATGTTGTATATGGAACCTCCAGAGTTAACTGATATATGTTGGACACATACAAAGTTTAA    | 1676 |
| Db  | 421  | CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGGACAAATTAGTTTAT   | 480  | Db                                    | 1441 | GCATGTTGTATATGGAACCTCCAGAGTTAACTGATATATGTTGGACACATACAAAGTTTAA    | 1500 |
| Qy  | 657  | TATTTTAACTTTTCAGAAAGAGATTTCAATGAAATTTAGGAGGGTCATTTGTCAGAAAC    | 716  | Qy                                    | 1677 | AAACGTGAAATATATAATTAAGGCCAATCAAAATTAACAATAACCCGCGGTGAAGAGTTAT    | 1736 |
| Db  | 481  | TATTTTAACTTTTCAGAAAGAGATTTCAATGAAATTTAGGAGGGTCATTTGTCAGAAAC    | 540  | Db                                    | 1501 | AAACGTGAAATATATAATTAAGGCCAATCAAAATTAACAATAACCCGCGGTGAAGAGTTAT    | 1560 |
| Qy  | 717  | AATGCTCAAGTATGTTATACCTACTTTTGCACAAGCTGCAAAATGTGCAGTTTATTTACTA  | 776  | Qy                                    | 1737 | TACCTTCAAAATTAATCTTGTCTAATGCGCTATACCTATGTAATAAAGGCACCTCATACAGGT  | 1796 |
| Db  | 541  | AATGCTCAAGTATGTTATACCTACTTTTGCACAAGCTGCAAAATGTGCAGTTTATTTACTA  | 600  | Db                                    | 1561 | TACCTTCAAAATTAATCTTGTCTAATGCGCTATACCTATGTAATAAAGGCACCTCATACAGGT  | 1620 |
| Qy  | 777  | TTAAGGGATGCAGTTCAATATAAAGCACAAATGGTTCCTAATTTTGAAGTGCAGAGAATGTA | 836  | Qy                                    | 1797 | GGGGATTTAATCCGTTTTTTAAAGAACAAATCAGAGTATAACGACGTTTATGTCAGGTGCG    | 1856 |
| Db  | 601  | TTAAGGGATGCAGTTCAATATAAAGCACAAATGGTTCCTAATTTTGAAGTGCAGAGAATGTA | 660  | Db                                    | 1621 | GGGGATTTAATCCGTTTTTTAAAGAACAAATCAGAGTATAACGACGTTTATGTCAGGTGCG    | 1680 |
| Qy  | 837  | AGATCGGAATTAATATCACCTAACAGTGGTGTGATTTTACCGGTGATTAATATGAGCGA    | 896  | Qy                                    | 1857 | GGAAATTAGATTGATTTAATAACAAACCTGCAGGACAAAGTTTACCGTATTCGTTTTCGT     | 1916 |
| Db  | 661  | AGATCGGAATTAATATCACCTAACAGTGGTGTGATTTTACCGGTGATTAATATGAGCGA    | 720  | Db                                    | 1681 | GGAAATTAGATTGATTTAATAACAAACCTGCAGGACAAAGTTTACCGTATTCGTTTTCGT     | 1740 |
| Qy  | 897  | TTAAATGCAAAACGGCAGAGTATACCAATTTATTTTATTTGTTATTCAGGTAGGTTTA     | 956  | Qy                                    | 1917 | TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGTTGGGGTTCA     | 1976 |
| Db  | 721  | TTAAATGCAAAACGGCAGAGTATACCAATTTATTTTATTTGTTATTCAGGTAGGTTTA     | 780  | Db                                    | 1741 | TATGCTGCAGATAAAGCTGCTTTCTTTAGTGTATATCTTTATCCAGGAGGTTGGGGTTCA     | 1800 |
| Qy  | 957  | AATCAGATAAAGACGGGGGGAACAGGTGTGACACTTGGTCGAAATTTAATAAATTTTCGT   | 1016 | Qy                                    | 1977 | AATCGTTTTGTATCGCTTGAAAAATCTTACTCTGGAATTTATGACGATTTTAAATAATAGT    | 2036 |
| Db  | 781  | AATCAGATAAAGACGGGGGGAACAGGTGTGACACTTGGTCGAAATTTAATAAATTTTCGT   | 840  | Db                                    | 1801 | AATCGTTTTGTATCGCTTGAAAAATCTTACTCTGGAATTTATGACGATTTTAAATAATAGT    | 1860 |
| Qy  | 1017 | AGAGAAATGACGTTGGCGGTATTTGGATATATTCGCTATATTTCCAACTTATGATTTTGAG  | 1076 | Qy                                    | 2037 | GATTTTAAATTCGCTGAAATTTATCACACCTCCATTAACCTAGTTTCAAAACATTCAGATGGAT | 2096 |
| Db  | 841  | AGAGAAATGACGTTGGCGGTATTTGGATATATTCGCTATATTTCCAACTTATGATTTTGAG  | 900  | Db                                    | 1861 | GATTTTAAATTCGCTGAAATTTATCACACCTCCATTAACCTAGTTTCAAAACATTCAGATGGAT | 1920 |
| Qy  | 1077 | AAATATCCATTCGCAACACATGTAGAGTTGACCTAGGGAAATTTATACAGATCAGTGGGA   | 1136 | Qy                                    | 2097 | GTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGTGGTTCTCGACAAATTTGAA    | 2156 |
| Db  | 901  | AAATATCCATTCGCAACACATGTAGAGTTGACCTAGGGAAATTTATACAGATCAGTGGGA   | 960  | Db                                    | 1921 | GTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGTGGTTCTCGACAAATTTGAA    | 1980 |
| Qy  | 1137 | TATTCATCGGGAACCTTATAGTTGGTTACGGAAATGGCCCTAATATCTTTTAATGGGTTAG  | 1196 | Qy                                    | 2157 | TTCTCTCCCAAGTAATACAACTTTTAGAATATAGAGGAGAAACGGGACCTTAGAAAAACA     | 2216 |
| Db  | 961  | TATTCATCGGGAACCTTATAGTTGGTTACGGAAATGGCCCTAATATCTTTTAATGGGTTAG  | 1020 | Db                                    | 1981 | TTCTCTCCCAAGTAATACAACTTTTAGAATATAGAGGAGAAACGGGACCTTAGAAAAACA     | 2040 |
|   |      |  |      | Qy                                    | 2217 | AAGAAACGGGTAACGATCTGTTTACCAATTTAA                                | 2249 |
|   |      |  |      | Db                                    | 2041 | AAGAAACGGGTAACGATCTGTTTACCAATTTAA                                | 2073 |

## RESULT 4

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US-10-781-979-6
; Sequence 6, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and
; FILE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10781.979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1686)
US-10-781-979-6.

Query Match      28.2%; Score 1686; DB 8; Length 1686;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2309 GTGAGTCTATGTTTACAGTAGTACGAAATAACGTTAAATAATAGAAACGACAGATTAT 2368
DB 1 GTGAGTCTATGTTTACAGTAGTACGAAATAACGTTAAATAATAGAAACGACAGATTAT 60

QY 2369 GAAATAGATCAAGCGGCCATTTCTATAGATGATGTACAGATGAAACAAATCCTCAGGAA 2428
DB 61 GAAATAGATCAAGCGGCCATTTCTATAGATGATGTACAGATGAAACAAATCCTCAGGAA 120

QY 2429 AAAATATGTTTGGGATGAAATATAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTA 2488
DB 121 AAAATATGTTTGGGATGAAATATAAACTGGCAAAACAACTTAGTCAGTCTCGTAATCTA 180

QY 2489 CTCGAAATCGAGACTTTCTGGGAATGATTTGGCAATTCGGTAATGATATATCATAGGA 2548
DB 181 CTCGAAATCGAGACTTTCTGGGAATGATTTGGCAATTCGGTAATGATATATCATAGGA 240

QY 2549 TCCAATAATCCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGCAGACATATAT 2608
DB 241 TCCAATAATCCTATTTTAAAGGAAATTTCTACAGATGCGTGGAGCAGCAGACATATAT 300

QY 2609 GGAACCTCTATTTCCAACTTATATCTGTCAAAAATAGATGAGTCTAAATTTAAACCATAT 2668
DB 301 GGAACCTCTATTTCCAACTTATATCTGTCAAAAATAGATGAGTCTAAATTTAAACCATAT 360

QY 2669 ACAGTTATCGAGTAGAGGTTTGGGAAGTAGTAAGATTTGAAATTTAAATGTTGTAACA 2728
DB 361 ACAGTTATCGAGTAGAGGTTTGGGAAGTAGTAAGATTTGAAATTTAAATGTTGTAACA 420

QY 2729 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTTCCAAATGATTTGGCCTATATGCGAG 2788
DB 421 CGTTACGGGAAAGAAATTTGATGCTATCATGAATGTTTCCAAATGATTTGGCCTATATGCGAG 480

QY 2789 CCTAATCCTTTGATGGAGATTAATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAAGG 2848
DB 481 CCTAATCCTTTGATGGAGATTAATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAAGG 540

QY 2849 TATCCTACCAACACAGATGATGCTCCCGATATGTATGTCATGCCCGCAAAATATAGAT 2908
DB 541 TATCCTACCAACACAGATGATGCTCCCGATATGTATGTCATGCCCGCAAAATATAGAT 600

QY 2909 AGAAGCATGTGAAGTGTACAGATCGTATCCATTTGATTTTTCATATTTGACACCGGAGAA 2968
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DB 601 AGAAGCATGTGAAGTGTACAGATCGTATCCATTTGATTTTCATATTTGACACCGGAGAA 660
QY 2969 GTAGATACAAATACAAATGTAGTATGTCTTATTAATAATTTCTAATCAGATGGA 3028
DB 661 GTAGATACAAATACAAATGTAGTATGTCTTATTAATAATTTCTAATCAGATGGA 720
QY 3029 TAGCGTACAGTAGGGAATCTAGAAATGTCATTGAGNAGGACCACTAACAGGTGAGCAATG 3088
DB 721 TAGCGTACAGTAGGGAATCTAGAAATGTCATTGAGNAGGACCACTAACAGGTGAGCAATG 780
QY 3089 GCACATGTGAAACAAAGGAAAGAAATGAAACAAACACATGAGAGAAAAACGTTGGGAA 3148
DB 781 GCACATGTGAAACAAAGGAAAGAAATGAAACAAACACATGAGAGAAAAACGTTGGGAA 840
QY 3149 ACACAAACAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTTATCAAAATGAACAA 3208
DB 841 ACACAAACAGCCTATGATCCAGCAAAACAGGCTGTAGATGCAATTTATCAAAATGAACAA 900
QY 3209 GAGTTACACTATCATATTTACTTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTCG 3268
DB 901 GAGTTACACTATCATATTTACTTTTAGATCATATTTCAAAACGCTGATCGACTGGTACAGTCG 960
QY 3269 ATTCCCTATGTATACCATTAATTGGTTACCGAATGCTCCAGGTATGAACTATGATATAT 3328
DB 961 ATTCCCTATGTATACCATTAATTGGTTACCGAATGCTCCAGGTATGAACTATGATATAT 1020
QY 3329 CAAGGTTAAACGACGATATCATGCAAGGTTATAATTTATATGATGACGAAATGTCATA 3388
DB 1021 CAAGGTTAAACGACGATATCATGCAAGGTTATAATTTATATGATGACGAAATGTCATA 1080
QY 3389 ACAAATGTTGACTTTTACCAAGGATTTACAGGATGCGACGCAACAGGAAATGCGCGGTA 3448
DB 1081 ACAAATGTTGACTTTTACCAAGGATTTACAGGATGCGACGCAACAGGAAATGCGCGGTA 1140
QY 3449 CAACAAATGGATGGAGCTTTCAGTATTTAGTTTCTATCAAAATGGAGCGCGGGGTATCTCAA 3508
DB 1141 CAACAAATGGATGGAGCTTTCAGTATTTAGTTTCTATCAAAATGGAGCGCGGGGTATCTCAA 1200
QY 3509 AACTTCGATGCTCAAGATCATCATGATATGTGTTACGTGTGATTCGCCAAAAAGAGGA 3568
DB 1201 AACTTCGATGCTCAAGATCATCATGATATGTGTTACGTGTGATTCGCCAAAAAGAGGA 1260
QY 3569 CTTGGAAAGGATGTGTAACGATGAGTGTGTTAAATGGAAAGCAGGAAACACATTAGTTTC 3628
DB 1261 CTTGGAAAGGATGTGTAACGATGAGTGTGTTAAATGGAAAGCAGGAAACACATTAGTTTC 1320
QY 3629 ACTTCTTGGAAAGAGGATATATGACAAAAACAGTAGAGGTATTTCCAGAAAGTGTATCGT 3688
DB 1321 ACTTCTTGGAAAGAGGATATATGACAAAAACAGTAGAGGTATTTCCAGAAAGTGTATCGT 1380
QY 3689 GTACGGAATGAAATAGGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTT 3748
DB 1381 GTACGGAATGAAATAGGAAACCGAAGGTACATTTTATATAGATAGCATCGAGTTGCTT 1440
QY 3749 TGTATGCAAGGATATGATTAACAAATTAATACCTGCACACCGGTAATATGATGAGCAAGT 3808
DB 1441 TGTATGCAAGGATATGATTAACAAATTAATACCTGCACACCGGTAATATGATGAGCAAGT 1500
QY 3809 TATAATGGAATTTATAATCAAAATACTAGCGATGTGTTATACCAAGGATATACAAACAAC 3868
DB 1501 TATAATGGAATTTATAATCAAAATACTAGCGATGTGTTATACCAAGGATATACAAACAAC 1560
QY 3869 TATAACCAAGACTCTAGTATATATGTAATCAAAATTTATATAAACAATGATGACCTGCAT 3928
DB 1561 TATAACCAAGACTCTAGTATATATGTAATCAAAATTTATATAAACAATGATGACCTGCAT 1620
QY 3929 TCCGGTTGACATGTAAACCAAGGCAATCTCTGGCTGTACATGTAATCAAGGATATAC 3988
DB 1621 TCCGGTTGACATGTAAACCAAGGCAATCTCTGGCTGTACATGTAATCAAGGATATAC 1680
QY 3989 CGTTAA 3994
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US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for Its Use
; FILE REFERENCE: 045600/274143
; CURRENT APPLICATION NUMBER: US/10782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-141-1

Query Match      14.3%; Score 855; DB 8; Length 2145;
Best Local Similarity 71.4%; Pred. No. 5.5e-169;
Matches 1255; Conservative 0; Mismatches 430; Indels 72; Gaps 7;

QY 49 AAATAATGGGTTATTTGTAGAAACATGTTACAGGAATACATGGGGTACTACGAATAT 108
DB 8 AAATATATAATGTTTTTTTGTAGAAACATGTTACAGGAATACATGGGGTACTACGAATAT 67

QY 109 ATAGAAAGACACCTAACATATATTTAGTGTCTTAAATAAAGACATATATAGGAG 168
DB 68 ATAGAAAGACACCTGGCATATATTTAGTGTCTTAAATAAAGACATATATAGGAG 127

QY 169 TGAAGAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAACTCCTCATCGA 228
DB 128 TGAATAATAATGAATCTTATCAAAATACAAATGAATATGAATCTTGGATGGTTCCTCGA 187

QY 229 ATACACAAATAGCCAAACAGATATCCTTTTGGAAATATCGGGATATGCTACTATGT 288
DB 188 ATACACAAATATGTCAACAGATATCCTTTTGGAAAGATCCAAATATATTTCTTATTA 247

QY 289 CTGGGAATGATGTCAGGGAATCTCAAGGATGAAATTTGGGAATCAGTCGAAACGATAA 348
DB 248 ACCTGGACGCTTGTGAGGAAGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATAG 307

QY 349 CAAGTATGGGATAAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAATA 408
DB 308 TAAGTATGGGACATACCTTATACAAATCTTGTAGAACCCGGTATAGGTGGAAATTCCTG 367

QY 409 CACTATTAACAATAAGGAAACCTAATTCGGAATATCGTCAAACTGTGTACGACTTTT 468
DB 368 TAATAATTTTCAATAATAAACAACCTCAATTCGCTCTTGTGTCATCTGTGGCAGCACTTT 427

QY 469 CTATATGTGATTTATTTATCTAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGATG 528
DB 428 CTATATGTGATTTATTTATCTAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGATG 487

QY 529 CGATTGCGAATTTTGACGGTAAATTTGAAATAATATAGAGAGTATTTCTTCTTATCTTG 588
DB 488 GGGTTCGAGATTTTGGGGTGAATGACTGCTTATCAAGATTTATTTCTTATTTCTTG 547

QY 589 GGGCTTGGCTTAAGACGGTAAACCACTTCAAAAGACAAATAATTTCTGATATCGGCAAT 648
DB 548 AGGATTTGGCTTACAG-----ATAAATCAATCTCTAAATAAATTTGCTGAGC 592

QY 649 TACTTTTATTTTAACTTTTCAAGAGATTTTCAATGAATTTCTAGAGGGTCAATGT 708
DB 593 TAGTTAAACAGTTTCCAAAGCAGCGGAAGAAGATTTCACTAAACTTTTAGCAGGGTCAAT 652

QY 709 CAAGAAACAAATGCTCAAGTATTTGTTATTAACCTACTTTTGCAACAGCTGCAAAATGTGAGT 768

653 CRAAGACAGAAAGCTGAAATATTTATTTACCTACGTATGTGCAAGCTGCAAAATGTGCAAT 712
769 TATTACTATTAAAGGATGCGATTCATATATAAAGCAATAGTGTCCCATTTTGGATGTCAG 828
713 TATTACTATTAAAGGATGCGATTCATATATAAAGCAATAGTGTCCCATTTTGGATGTCAG 772
829 AGAATGTAGATCGGAATTAATATACCTTAACAGTGTGTGTGATTTTACCGGTGATTAAT 888
773 TGTATCGAGGTGAGGAGAA-----CTGATTGTA 802
889 ATGAGCGATTTAAATTCGAAACCGGAGAGTATACCAATTTATTTTATATTTGGTATCAGG 948
803 ACAGCGGTTTAAAGCGGAAATAAAGAGGTATATAATTTATTTGAGGTGATTAACA 862
949 TAGGTTTAATCAGATATAAAGCGGGGAGACAGTCTGACACTTGTGCGAAATTTAATA 1008
863 AGGGTTTAGATCAGATTAAGAAGCGGGGTACAGTGTCTGAAGTTTGTGTCGAAATTTAATA 922
1009 AATTTCTGAGAGAAATGACGTTTGGCGGTATTTGGATATTTATCGCTATATTTTCCAACTTATG 1068
923 AATTTCTGAGAGAAATGACGTTTGGCGGTATTTGGATATTTATTTTCCAACTTATG 982
1069 AATTTGAGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGATG 1128
983 AATTTGAGAGAAATATCCATTTAGCAACAGGTAGAGTTAACTAGGGAAATTTATACAGATC 1042
1129 CAGTGGGATATTCATCGGGAACTTATAGTTGGTTACGGAATTTGGCCCTAATATCTTTTAATG 1188
1043 CAGTGGGATATTCAGGGGAAATTTATGGTTGGGAAACGGTTTT-----TAGCTTTAAAT 1096
1189 GGTTAGAGCTAATGCAACACCGGGACCTGGTTTACTTACTTGGCTTACGCAAAATAGGTA 1248
1097 CGGTAGAGCAATGGAACACCGGGACCTGGTTTACTTACTTGGCTTCAAGCTATAGATA 1156
1249 TATATATGAGTATGTT-----TCGAGATATTTTGGCGGCTGGGTAGGAACTCGTC 1299
1157 TATATAGTCAATCTTATTTATCTTACGCTTGGTTATCTTAGTGGCTGGGGGAACTCGTC 1216
1300 ATTTGAGAGACTACAAAGGGTAAAGGTTATTTTCAACGATATGCTCGGAACTACAGATA 1359
1217 ATTTATGAGACTTCAAAAGGGTAAAGGTTATTTTCAAGCTATGCTCGGAACTACAGATA 1276
1360 ATGATCTAGTAAATTTGATTTTTCAGATGCGGATGATATATAAATTTACTTCAATTAAGTA 1419
1277 ATAAATCCAGTAAATATTTTGGCAATACCGATATATTTTAAATTTATTTTCAATTAAGTA 1336
1420 TCATG---AACCTAGTAGGAGAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGCAG 1476
1337 GATATGCAATGCAACCGTTTGTGGGTATTTCAATCCACGGCATCTTGTTCACGTGTCAG 1396
1477 ATTTTCGTAGGGTAGGGGACCTGATTTAAATTTATGATGAGGTAAATATAGGCTAAGCA 1536
1397 AATTTTTCGCAACACACTAAATATCTTCTGATGAGGTAAACAGTCTTGGGTA---CT 1453
1537 GGATGCAATTCGATCTAGCTTCCCACTTGTATTTGCACTCTAA-----TGGTGTAGAG 1590
1454 CACAGCAATTAATGATCTGTTTACAGGTATTTAAATAGGATCTTACCACTAGTCTGACAA 1513
1591 GACCTCTCATAGATTTTCAAAATGGGCAATGTTGTGATATGGAATCTCAGAGTTTAAAG 1650
1514 ATTTCTCTCATAGATTTTCAAAATGGGCAATGTTGTGATATGGAATCTCAGAGTTTAAAG 1573
1651 TATAAGTTGGGACATACAAAGTTTAAAGCGTGAATAATATAATTTGAAGCGCAATCAATTA 1710
1574 TATTTGGTTGGACACATACAGTAAAGGAAAGATAATCGAATTTTATCCAGATAAATTA 1633
1711 CACAAATACGGGGTGAAGATTTTACTTTCAAATTTATCTTGTCTAATGCTATACCT 1770
1634 CGAAATTCCTGAGTAAAGGCTTTTGGCCCTACAGCAGGTACAGGATATGCGAGGTT 1693
1771 ATGTAATAAAGGCACT 1787
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; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2019)  
US-10-782-141-2

Query Match 12.5%; Score 747.2; DB 8; Length 2019;  
Best Local Similarity 69.8%; Pred. No. 2.5e-146;  
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

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Qy 168 GTGAAAGATGAGTCCATATCAAAATATAAAATGAATATGAATATTTGGAAATCCTCATCG 227
Db 1 GTGAAATATGAATCTTATCAAAATACAAATGAATATGAATTTCTGGATGGTTCCTCG 60
Qy 228 AATAACAAATACGCCAAACAGATATCCTTTTGGCAAAATAAATCGGATATGTTCTACTATG 287
Db 61 AATAACAAATATGTCAAAACAGATATCCTTTTGGCAAAAGATCCAAATATATTTCTCTATT 120
Qy 288 TCTTGGAAATGATGTGAGGGAATCTCATGGATGAATTTGGGAATCAGTCGAAACGATA 347
Db 121 AACCTGACGCTGTGTGAGGGAAGCCATGCAAGATACGTGGGAATCAGTCTCGGATATA 180
Qy 348 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACTAGTTTGGGTGGAATTAAT 407
Db 181 GTAACATTTGGGACATACCTTATACAAATCTTGTAGAACCCGGTATAGTGGAATTCCT 240
Qy 408 ACATATTTCAATAATAGGAAACCTAATTTCCGACTAATCGTCAAACTGTGTGAGCACTT 467
Db 241 GTAATATTTCAATAATAAACAACCTAATTTCCGCTCTTCTGGTCAATCTGTGGCAGCACT 300
Qy 468 TCTATATGATATTTATATCTATTAATTCGTAAGAGGTAGCCATAGTGTATTTAAGTAT 527
Db 301 TCTATATGATTTAGTATCTAATAATTCGTAAGAGGTAGACGAGAGCGGTGTTAAGTGAC 360
Qy 528 GCGATTGCGATTTTGACGGTAAATTTGAAATAATATAGAGAGTATTAATCTTTCTTATCTT 587
Db 361 GGGTTGCGATTTTGAGGGTGAATGACTGCTTTATCAAGATTAATTAATCTTCAATATCTT 420
Qy 588 GGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATTAATCTGATATCGGACAA 647
Db 421 GAGGATTTGGCTTACAG-----ATAAATCAATCCTAAATAAATCTTGGTAC 465
Qy 648 TTAGTTTATTTATTTAACTTTTCAAGAGATTTCAATGAATTTCTAGAGGGTCAATTG 707
Db 466 GTAGTTTAAACAGTTTCAAGACCGGGAAGAAGATTTTCACTAAACTTTTAGCAGGGTCATTA 525
Qy 708 TCAAGAAACAATGCTCAAGTATTTGTTATTAATCTTCTTCAAGCTGCAAAATGTCAG 767
Db 526 TCAAGACAGAAAGCTGAAATATTTATTTCCCTACGTAATGTAAGCTGCAAAATGTCAT 585
Qy 768 TTATTAATAATTAAGGATGAGTCAATATAAAGCAAAATGTTTCCCATTTTGAAGTGA 827
Db 586 TTATTAATAATTAAGGACCGAGTTAAATATAAATAAAGAAATGAGGAGCTAGTGTGTCACCG 645
Qy 828 GAGAAATGATAGTCGGAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTAC 887
Db 646 TTGTTATCCAGGGTCAGGAGAA-----CTGATTTGT 675
Qy 888 TATGAGCGATTAATAATGCAAAACCGGACGAGTATACCAATTTATTTGTTTATATTCGTATCAG 947
Db 676 AACGAGCGTTAAAGCGGAAATAAAGAGATATTAATTTATTTGTAGGGTGGTATAAC 735
Qy 948 GTAGGTTTAAATCAGATATAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTAAT 1007
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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Db 736 AAGGGTTTAGATCAGATAAGACAGCGGGGTACAAGTGTGTAAGTTTGGTCGAAATTTAAT 795
Qy 1008 AAATTTTCTAGAGAAATAGCTTTGGCGGTATTGGATATTATTCCTATATTTTCAACTTAT 1067
Db 796 AAATTTTCTAGAGAAATAGCTTTGGCGGTATTGGATATTATTTCTATATTTTCAACTTAT 855
Qy 1068 GATTTTGGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAATTTTATACAGAT 1127
Db 856 GATTTTGAATAATATCCATTTAGCAACAGGTAGAGTTAACTAGGGAATTTTATACAGAT 915
Qy 1128 GCAGTGGGATATTCATTCGGGAATCTATAGTTGGTTACGGAATTTGGCTTAATCTCTTAAT 1187
Db 916 CCAGTGGGATATTCAGCGGGAATTTATGTTGGGAACGGTTTTT-----TTAGCTTTAAT 969
Qy 1188 GGGTTAGAGCTTAATCGAACAACGGGACCTGTTTGTAGTTTACTTTGGCTTAGCAAAATAGGT 1247
Db 970 TCGGTAGAGCAAAATCGAACACCGGGACCTGGTTTGTAGTTTACTTTGGCTTCAAGCTATAGAT 1029
Qy 1248 ATATATAATGAGTATGTT-----TCGAGATATTTTGGCGCTGGGTAGGAACCTCGT 1298
Db 1030 ATATATAGTCAATCTATTAATCTTCAAGCTTGGTTATCTTAGTGGCTGGGGGGAACCTCGT 1089
Qy 1299 CATTTAGAGACTACACAAAGGGTAAACGGTATTTTTCAACGATATGTTCTGGAACCTACGAGT 1358
Db 1090 CATTTAGAGACTTCAAAAGGGTAAACGGTCTTTTCAACGATATGTTCTGGAACCTACGAGT 1149
Qy 1359 AATGATCTAGCTAATATGATTTTTCAGATGCGGATGATATATAAATTTACTTCAATAGCT 1418
Db 1150 AATAATCCACGTAATATTTTGGCAATACCGATATATTTAAATTTATTTTCAATAGCT 1209
Qy 1419 A---TCATGAACCTTAGTAGGAGACTACCGCTAGACAGAGTATCGTGTTCCTCAAAAGGCA 1475
Db 1210 AGATATGCAATGCAACCGTTTGTGGGTATTTCAATCCACGCAATCTTGTTCACGTGCA 1269
Qy 1476 GAATTTCTGAGGTAGGGGACCTGATTTAAATTTATGATGACAGGTAAATTAATGGCTTAAGC 1535
Db 1270 GAATTTTTCGACAACTAAATACTTTTCTGTATGAGGTAAACAGTTCCTGGG---TAC 1326
Qy 1536 AGGTGACAAATTTGAATCTAGTTCCTCACTTGT-----ATTGCACTCTAATGGTGTAGA 1589
Db 1327 TCACAGACAAATTTGATCTGTGTTACCGGATTAATAAGGATCTTACCACCTAGTCGTACA 1386
Qy 1590 GGAACCTCTCATAGATTTCAAAATGGCGATGTTGTTATATGGAACCTCCAGAGTTAAC 1649
Db 1387 AATTACTCTCATAGATTTCAAAATGGCGATGTTGTTCAAAATGAAACCTCCAGAGTTAAC 1446
Qy 1650 GTATATGTTGGACACATACAAGTTTAAACGCTGAAATATATAATTTGAAGCCCAATCAATTT 1709
Db 1447 GTATTTGGTTGGACACATACAAGTATGAAATAAGATATAATCGAATTTTATCCAGATAAATTT 1506
Qy 1710 ACACAAATACCGCGGTGAGAGTTTATACCTTCAAAATTTATCTTGTCTAATGCTATACC 1769
Db 1507 ACGCAAAATTCCTGCAATGAAAGCTTTTGGCCCTACCGAGGTACAGGATATGCGAGGTT 1566
Qy 1770 TATGTAATAAAGGCACT 1787
Db 1567 TAGTCACAGCTGGGCT 1584
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## RESULT 9

US-10-782-141-4  
; Sequence 4, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; TITLE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141

```
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
US-10-782-141-4

Query Match      12.4%; Score 739.8; DB 8; Length 2010;
Best Local Similarity 69.7%; Pred. No. 8.9e-145;
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;

QY 177 ATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCGAATAACACA 236
Db 1 ATGAATTTCTTATCAAAATAACAAATGAATATGAATTTCTGGATGGTTCCCGGAATAACACA 60

QY 237 AATACGCCAAACAGATATCTTTTGCAGAAATAATCGGGATATGCTACTATGCTTGGAAAT 296
Db 61 AATATGTCAACAGATATCTTTTGCAGAAATGATCCAAATATATTTCTTAACTTGGAC 120

QY 297 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTTCGAAACGATAACAAAGTATT 356
Db 121 GCTTGTGAGGGAAGCCATGGCAAGATACGTTGGGAATCAGTCTCGGATATAGTAATATT 180

QY 357 GGGATAAATCTTATAGAGTTGTGATAGAACCTAGTTTGGGTGGGAATTAATACATATTA 416
Db 181 GGGACATACCTTATACAAATCTTTGCTAGAACCCGGTATAGGTGGGAATTCCTGTAATATT 240

QY 417 TCAATATAGGAAACCTAATTCGGACTAATCGTCAAACTGTGTCAGCACCTTTCTATATGT 476
Db 241 TCAATATAAACAACTCATCTCGTCTTCTGGTCAATCTGTGGCAGACCTTTCTATATGT 300

QY 477 GATTATTAATCTATAAATCGTAAAGAGGTAGCCGATAGTGTTTTAAAGTATGATCGAATGCA 536
Db 301 GATTATAGTATCTATAATTCGTAAGAGGTAGACGAGAGCGGTGTTAAGTACGGGGTTGCA 360

QY 537 GATTTTGACGGTAAATGAAATTTATAGAGAGTATATCTTTCTTATCTTGGGGCTTGG 596
Db 361 GATTTTGGGGTGAATATGACTGCTTTATCAAGATTATATCTTCTTATCTCTGAGGATTGG 420

QY 597 CTTAAAGACGGTAAACCACTTTCAAAAGACAAATAATTCGATATCGGACAAATTTAGTTTAT 656
Db 421 CTTACAG-----ATAATCAATCCTTAAAAAACCTTGCTGACGTAGTTAAA 465

QY 657 TATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGGTCATTTGTCAAGAAAC 716
Db 466 CAGTTCCAGACCGGGAAGAAGATTTTCACTAAACTTTTAGCAGGGTCATTTATCAAGACAG 525

QY 717 AATGCTCAAGTATGTTATTTACCTACTTTTTCGACAAAGCTGCAAAATGTCAGTTTACTTA 776
Db 526 AAGCTGAAATATTTATTTATGCTGCTATGTCGTAAGCTGCAAAATGTCATTTTATTTACTA 585

QY 777 TTAAGGATGTCAGTTCAAATAAAGCAGCAATGTTCCCATTTTGTGATGTCAGAGATGTA 836
Db 586 TTAAAGGACGCGAGTTAAATATAAAGAAATGGGACGTAGTGTGTCACCGTTGTATCCA 645

QY 837 AGATCGGAATTAATATCACCTAACAGTGGTGTGATTTTATCCGGTGATTACTATGAGCGA 896
Db 646 GGGTCAGGGAGAA-----CTGATTGTAACGAGCGG 675

QY 897 TTAAATGCAAAACGCGAGATATACCAATTAATTTTATATTTGGTATCAGGTAGGTTTA 956
Db 676 TTAAGGCGGAAAATAAAGAGATGATACATTAATTTGTAGGGGTGATTAACAAGGGGTTTA 735

QY 957 AATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTTAATAAATTTTCTG 1016
Db 736 GATCAGATAGACAGGGGGGTACAGTGTGAGTTTGGTCGAAATTTTAATAAATTTTCTG 795
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QY 1017 AGAGAAATGACGTTGCGGTAATTTGATATATCGTATATTTCCAACTTATGATTTTGAG 1076
Db 796 AGAGAAATGACGTTGCGGTAATTTGATATATTTGCTATATTTCCAACTTATGATTTTGAA 855

QY 1077 AATATATCCATTTGCCAAACACATGTAGAGTTGACTAGGGAATTTATACAGATCCAGTGGA 1136
Db 856 AATATATCCATTTAGCAACCAAGTGTAGAGTTAACTAGGGAATTTATACAGATCCAGTGGA 915

QY 1137 TATTCATCGGGAACTTATATAGTTGGTTACGGAATTTGGCCCTAAATCTTTTAAATGGGTAGAG 1196
Db 916 TATTCAGGGGAAATTTATGGTTGGGAACGGTTTT-----TTAGCTTTAAATTCGGTAGAA 969

QY 1197 GCTAATGGAACACGGGACCTGGTTTGTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT 1256
Db 970 GCAATATGGAACACGGGACCTGGTTTGTAGTTACTTGGCTTCAAGCTATAGATATATAGT 1029

QY 1257 GAGTATGTT-----TCGAGATATTTTGGCGCTGGGTAGGAACCTGCTCATTTAGAA 1307
Db 1030 CATTTCTATTTAATCTTCAAGCTTGTATCTTATAGTGGCTGGGGGGAACCTGCTCATTTAGAA 1089

QY 1308 GACTACACAAAGGGTAAACGGTATTTTCAACGATATGTCTGGAATCTACGAGTAAATGATCTA 1367
Db 1090 GACTTCAACAAAGGGTAAACGGTCTTTTCAACGATATGTCTGGAATCTACGAGTAAATGATCTA 1149

QY 1368 CGTAATATTTGATTTTTCAGAAATGCCGATGTATATAAAATTTACTTCAATAGCTA---TCATG 1424
Db 1150 CGTAATATTTTGGCAATACCGATATATTTTAAATTTATTTTCAATAGCTATAGATATGCA 1209

QY 1425 AACCTAGTAGGAGACACTACCGCTAGACACAGATATCGGTTCGAAAGCAGATTTTCGT 1484
Db 1210 ATGCAACCGTTTGGGTATTTCAATCCACGGCATCTTGTTCACGTGTCAGGAATTTTCT 1269

QY 1485 AGGGTAGGGGACCTGATTTAAATTTATGATGACGAGTAAATTAAGGCTTAAGCAGAGTATGCA 1544
Db 1270 CCGACAAACATTAATTTACTTTCTGTATGAGGTAAACAGTTCTGGG---TACTCACAGACA 1326

QY 1545 ATTGAATCTAGCTTCCACTTGT-----ATTGCACTCTAATGGGTGTAGAGGACCTCT 1598
Db 1327 ATTGAATCTGTGTTACCAGGTATTAATGAAGATCTACCACTAGTCTGACAAATTTACTCT 1386

QY 1599 CATAGTATTAATCAAAATGCGGCATGTTGTATATGGAATCCAGAGTTAAACGTATATGTT 1658
Db 1387 CATAGTATTAATCAAAATGCGGCATGTTGTCAAAATGAACCTCCAGAGTTAAACGTATATGTT 1446

QY 1659 TCGACACATACAAAGTTTAAACGCTGAAATATAATTTGAAGCCAAATCAAAATTTACAAAATA 1718
Db 1447 TCGACACATACAAAGTATGAATAAAGATTAATCGAATTTATCCAGATATAAATTTACGCAAT 1506

QY 1719 CCGGCGGTGAAGAGTATTTACCTTCAAAATTTATCTTGTAAATGCTTATACCTATGTAATA 1778
Db 1507 CCGGAGTAAAGAGCTTTTGCCCTACACGAGGTACAGGATATGCGAGGAGTTACGTCACA 1566

QY 1779 AAGGCACCT 1787
Db 1567 GCTGGGCT 1575

RESULT 10
US-10-120-544A-3
; Sequence 3, Application US/10120544A
; Publication NO. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Mabao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
```

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FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/10/120,544A
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4359
TYPE: DNA
ORGANISM: Bacillus popilliae
FEATURE:
NAME/KEY: CDS
LOCATION: (282)..(4229)
US-10-120-544A-3

Query Match
Best local Similarity 59.0%; Score 390; DB 5; Length 4359;
Matches 815; Conservative 0; Mismatches 535; Indels 54; Gaps 5;

QY 2292 AATAAGCGAAAGGTTGTGAGTCCCTATGTTTACAAGTAGTACGAAATAACGTTAAAA 2351
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2320 AAAAAGCAAGAAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAGGCGCTAAAG 2379
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCATTTCTATAGAAATGATGTCAGATG 2411
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2380 AAGCAGACCGATTATGAGATCGATCAAGCCGCAACGGTGGTGGATGTTATATCGGATG 2439
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2412 AACAAATCTCAGGAAAAAATAATGTTATGGATGAAATPAAACTGGCAAAACAACTTA 2471
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2440 ---AGTGTGACATGAAAAATGATCCTGTTAGTGAAGTAAATATGCAAAACAACTCA 2496
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2472 GTCAGTCTGTAATCTACTCAAAATGGACACTTTTCT----- 2509
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2497 GCCAAGCCGCAATTTACTGCTCAATGGGAATTTTCGATGATCTATATCCAGCTCTGGAGA 2556
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2510 ---GGGAATGATGGACATTCGGTAATGATATATCATAGGATCAATATATCTTATTTTA 2567
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2557 GGGAGATCCATGGAAACAGTCCGCAATGTTAGTCCGTCAGATTAACCCGATTTTAA 2616
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2568 AAGGAAATTTCTACAGATCGGTGGAGACGACGACATATATGGAAC-----TCTATTTTC 2621
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2617 AAGGCCATTATCTCAGTATGGCGGTGGAAACGATATTGAGGCCACCAATGATACCTTCC 2676
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2622 CAACCTATATCTCTCAAAATAGATGAGTCTAAATTAATTAACCATATACAGTTATCGAG 2681
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2677 CCACGTATGTTCTATCAAAATATAGACGAAGCCAAATTAAGCCATATACACGGTATAAAG 2736
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2682 TAAGAGGTTTGTGGGAAGTAGTAAAGATTGGAATTTAATGTAACACGTTACGGGAAG 2741
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2737 TGGCGGGTTTGTGGTAGCAGAAAGCTCTAGAGCTGTTGGTTACACGCTATAATGAAG 2796
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCTTATATGACGCTTAATCTTTCAT 2801
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2797 AAGTCGATCGATTTTAGATGTACCGGATAATATCCGCAATGCGCGACTCTCTGTGCG 2856
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2802 GTGAGATTTATCGTGTGAATCATCGTC-----TCAGTATGTAGCGCAAG 2846
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2857 GTGAATTTGATGATGCAAGCCCTATTTCGTATCCACCTTTTACCTCCAGAAATGTAACCCCTG 2916
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2847 GGTATCTACCAACACAGATGATATGCTCCCATATGATGATGATGATGATGATGATGATGATG 2906
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2917 AGTTTAAATCATGATGCAACCATCTCTTGGCACCACCAATCATGATGATGATGATGATGATG 2976
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2907 ATAGAAAGCATGTGAAGTGTGACGATCGTATCCATTTGATTTTTCATTTTGAACACCGGAG 2966
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2977 ACAGAAACACCGCAATGTATCAAGCGCATCAATTTGATTTCCATTTGATGATGATGATG 3036
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2967 AAGTAGATCAAAATCAAAATGTTAGTATGATGCTTTTATTAATAAATTTCTTAATCCAGATG 3026
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3037 CAATCGATCTGGTGAAGATTGGGCAATTTGGGATGATCTTCAAAATCTGTGCCACAGATG 3096
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 3027 GATACGCTACAGTAGGAATCTAGAAGTCAATTGAAGAAGGACCACCTAAACAGGTGAAGCAT 3086
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3097 GTTACGCAAGCTTAGATGATTTGGAAAGTATTGAAGAAGGAGCGCTGGGTGTCGAAGCAT 3156
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3087 TGGCAGATGTGAACAAAAAGGAAAAATGGAACAACAACATGGAAGAAAAACGTTGGG 3146
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3157 TAGAACTTGTCAAGAAAAAGAAAAATGGAAGATCAGAAAGGAGCAGCATGTTTCG 3216
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3147 AAACACAACAGCCTATGATCCAGCAAAACAGCCTGTAGATGATTTATTACAAA----- 3201
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3217 AAACGAAACACAATATGATGGCGCCAAACACCGGTGATGGCGTTATTTCACAAACACG 3276
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3202 -TGAACAAGAGTTACACTATATATTACTTTAGATCATATTTCAAAACGCTGATCGACTGG 3260
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3277 GCTATGAAAAATTTGAAGTTGAAACCAACCATCTCCAAATTTTGTATGCTGATCATCTCG 3336
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3261 TACAGTCGATTCCTATGATATACCATTAATTTGGTTACCGAATGCTCCAGGTATGAACCTATG 3320
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3337 TGCAGTCGATTCCTTATGATATAATAAATATGTCACCGAAGTTCCAGGTATGAATTAACG 3396
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3321 ATGTATATCAAGAGTTAAACGCAAGTATCATGCAAGGTTATATTTATATATGATGACAGAA 3380
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3397 AACTCTATACAGAGCTAAACACTCTCGTTTCAAGATCGTTTCTATCTATATATGACACGCG 3456
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3381 ATGTCTATAACAAATGTGACTTTTACACAAGGATTACAGGATGCGCAACAGGAATG 3440
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3457 ATCTGATTAATAAATGGCGCTTTAGCAATGGGCTTATGTTGGCAGGCTACCCCGCATG 3516
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3441 CCGCGGTACAAACAATGGAATGGAGCTTCAGTATTTAGTTCTTATCAAAATGGAGCGCGGGG 3500
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3517 CACGAGTGGAAACAAGAAATATAGAAATCTGTACTGCTGCCAAATGGGATGCCAATG 3576
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3501 TATCTCAAAACTTGCATGCTCAAGATCATCATGATGATGATGATGATGATGATGATGATG 3560
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3577 TGTGCGAAGATCTTTGTATCGAACCAATCGCGGTTATGTTTTCGCTGTACACGCGAGAA 3636
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3561 AAGAAGGACTCTGAAAGGATGTAACGATGATGATGATGATGATGATGATGATGATGATGATG 3620
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3637 AAGAAGATCGGAGGCTGCAATTTACCTTCAGTACTGTGCAAAACCATGTCGACAGC 3696
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3621 TTAAGTCTACTTCTTCGCAAGAG 3644
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3697 TGAGCTTTACTTCTTCGATATAG 3720
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 11
US-11-091-654-3
Sequence 3, Application US/11091654
Publication No. US20050172355A1
GENERAL INFORMATION:
APPLICANT: TANAKA, Masao
APPLICANT: YOKOYAMA, Tomoko
APPLICANT: AOYAGI, Moriochi
APPLICANT: HASEGAWA, Makoto
APPLICANT: EHARA, Gaku
APPLICANT: KIMURA, Masaharu
APPLICANT: NISHIHASHI, Hideji
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
TITLE OF INVENTION: polynucleotide encoding the same
FILE REFERENCE: OP1335
CURRENT APPLICATION NUMBER: US/11/091,654
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: JP 2001-115754
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: JP 2001-203463
PRIOR FILING DATE: 2001-07-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 4359
TYPE: DNA
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|    |      |   |      |
|----|------|---|------|
| Qy | 2341 | TACGTTAAATAATAGAAACGACAGAGTATTAGAAATAGATCAACGGGCCAATTTCTATAGAAATG | 2400 |
| Db | 2073 | TGCCTTACAGACAAGTGTAAACGGGATTTACAGTGAATCAACGGCGCAAATTTAGTAGAATG    | 2132 |
| Qy | 2401 | TATGTCAGATCAAAACAAATCCTCAGGAAAAATAATGTTATGGCATGAAATAAACCTGGC      | 2460 |
| Db | 2133 | CCTATCCGATGAGTTATACCCAAATGAAAAACGAAATGTTATGGGATGCAGTGAAAGAGGC     | 2192 |
| Qy | 2461 | AAAAACAATTAGTCAGTCTCGTAAATCTACTCCAAAAATGGAGACTTTTTCTCGGAAATGAT--  | 2518 |
| Db | 2193 | GAACGACTTGTTCAGGCACGTAACCTTACTCCAAGATACAGGCTTTAATAGGATTAATGG      | 2252 |
| Qy | 2519 | -----TGGACATTCGGTAATGATATATCATAGGATCCAAATTAATCCTATTTTTAA          | 2568 |
| Db | 2253 | AGAAAAACGGATGGGACGGGAAGTACGGGAATCGAGGTTGCGGAAGGAGATGTTCTGTTTAA    | 2312 |
| Qy | 2569 | AGGAAAAATTTCTACAGATGCGTGAGCAGCAGACATATATGGAATCTTATTTCCAACTTA      | 2628 |
| Db | 2313 | AGATCGTTCGCTTCGTTTGACAAGTGCAGAGAGATTTGATACAGAAACATATCCACGTA       | 2372 |
| Qy | 2629 | TATCTGTCAAAAAATAGATGAGTCTAAATTTAAAAACCATATACAGCTTATCGAGTAAGAGG    | 2688 |
| Db | 2373 | TCTCTATCAACAAATAGATGAATCACCTTTTAAAAACCATATACAGATATAAATCTAAAGG     | 2432 |
| Qy | 2689 | GTTTGTGCGGAAGTAGTAAGAAATTTGAAATTTAATCGGTAACAGTTACGGGAAAGAAATTTGA  | 2748 |
| Db | 2433 | TTTTATAGGAAGTAGTCAAGATTTTAGAGATTTAAATTAATACGTATCATCGGCAAAATCAAT   | 2492 |
| Qy | 2749 | TGCTATCATGAATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCCTTTCATGTGGAGA     | 2808 |
| Db | 2493 | CGTCAAAAATGTACAAGATTAATCTTTGCCAGATGTACTCCCTGTCAAAATTTCTTTGGTGG    | 2552 |
| Qy | 2809 | TTATCGCTGTGAATCATCGTCTCAGTATGTGAGCCAAGGGTATCCTACACCAACACAGATGG    | 2868 |
| Db | 2553 | GATCGATCGCTGCAGTGAGCAACAGTATGTAGCGCGAAATTAGCTCTCGAAACATATGG       | 2612 |
| Qy | 2869 | ATATGCTCCCGATATGTATGATGATGCCCGCAAAAATATAGATAGAAAGCATGTGAAGTGTCA   | 2928 |
| Db | 2613 | AGAAAAATGGAAATATGTCTTCT-----                                      | 2634 |
| Qy | 2929 | CGATCGTCAATCCATTTTCATTTTCATATTGACACGGAGAAGTAGATACAAATACAAATGT     | 2988 |
| Db | 2635 | -GATTCCTCATGTCATTTCTTTCCATATTGATACAGGTGAAATAGATTGAAATGAAATATC     | 2693 |
| Qy | 2989 | AGGTAATTGATGTCCTTATTAATAAATTTCTAAATCCAGATGGATAGCTACAGTACGGGAATCT  | 3048 |
| Db | 2694 | AGGAAATTTGGTGGTATTTAAATTCGACAAACAAATGGATAGCAACACTAGAAATCT         | 2753 |
| Qy | 3049 | AGAAGTCATTGAAGAAGGACCACTAACAGGTGAAGCATTTGGCCATGTGTGAACCAAAAGGA    | 3108 |
| Db | 2754 | TGAATTCGTAGAGAGGGGCGCATTTGTCAAGGGGAAACATTAGAACGAGCAACAACAAGA      | 2813 |
| Qy | 3109 | AAAGAAATGGAAACAACACATGGAGAAAAACGTTGGGAAACAACAACAGCCTTATGATCC      | 3168 |
| Db | 2814 | ACAAATGGAACAGACAAAATGGCAAAAACGTGGGGCATCAGAAAAGCATATTATGTC         | 2873 |
| Qy | 3169 | AGCAAAACAGGCTGTAGATGCAATTTATTAACAATGAAACAAGAGTTACACATCATATTAC     | 3228 |
| Db | 2874 | AGCAACGACAGCCATTTGATCGTTTATTCGCAAGTATTCAGACCAAAAATTTAATTCCTGG     | 2933 |
| Qy | 3229 | TTTAGA-----TCATATTCAAAACGCTGATCGATGGTACAGTCGATTTCCCTATGTATA       | 3282 |
| Db | 2934 | TGTAGAAATGTCAGATATGTTGGCAGGCCAAAACCTTGTACAGTCCATTCTCTACGTATA      | 2993 |
| Qy | 3283 | CCATAATTTGGTTACCGAATGCTCCAGGTATGAACATATGATGTATATCAAGAGTTAAACGC    | 3342 |
| Db | 2994 | TAATGATGCGGTTACCGAATAATCCCTGGAAATGAACTATACAGATTTTACAGAGTTAACAA    | 3053 |
| Qy | 3343 | ACGTATCATCGAAGGTTATATAATTTATATGATGACGAAATGTCTATACAAATTCGTACCTT    | 3402 |
| Db | 3054 | TAGACTCAACACAGCATGGAATTTGTATGATCTTCGAAATTTGCTATATCCAAATGGAGATT    | 3113 |
| Qy | 3403 | TACAAGGATATACAGGATGGCACGCAACAGGAAATGCGCGGTACAAACAAATGATGATG       | 3462 |

RESULT 13

US-10-089-678-3

; Sequence 3, Application US/10089678

; Publication No. US20030017967A1

; FACTICATION NO: 0320  
; GENERAL INFORMATION:  
; GENERAL INFORMATION:

;; GENERAL INFORMATION:  
;; APPLICANT: ASANO, shinichiro

;  
; AFFICIAN: ASANO, SHIMICHIRO  
: TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY. DNA ENCODING THE PROTEIN

; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCO  
; TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

; TITLE OF INVENTION: N  
 : FILE REFERENCE: Q68821

FILE REFERENCE: Q68821  
CURRENT APPLICATION NUMBER: IIS/10/088 678

; CURRENT APPLICATION NUMBER: US/10/089,67  
 ; CURRENT FILING DATE: 2002-05-02

; CURRENT FILING DATE: 2002-05  
: PRIOR APPLICATION NUMBER: JP

; PRIOR APPLICATION NUMBER: JP 2000-236140  
 : PRIOR FILING DATE: 2000-08-03

; PRIOR FILING DATE: 2000-08-03  
: PRIOR APPLICATION NUMBER: PCT

; PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SE

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; SOFTWARE: Pat

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; SEQ ID NO 3

; LENGTH: 3690

; TYPE: DNA

Query Match 6.44: Score 380.8: DB 5: Lenath 3690:

Query Match 6.4%; Score 380.8; DB 3  
Best Local Similarity 55.4%; Pred. No. 3, 7e-69;

BEAC LOCAL SIMILARITY 55.4%; Pred. NO. 3./e-69;  
Matches 881: Conservative 0: Mismatches 622: Indels 87: Gaps 4:

2221 ACGCGGTGAACGATCTGTTTACCAATTAAACAAAAATAATTTACTAGAAATAGGTGGTATT 2280

QY 2221 ACGGGTGAACGATCIGTITACCAATATAAACAAAAATTAATTTACTAGAAATAGGTGGTATT 2280

2139 AGGAGGAGAGTTTATGTAGATAGTTCCGACCTTATTCGGTATATGCAACATTTTCATAC

DB 2139 AGGAGGAGAAGI<sup>1</sup>TATAGTAGATAAGTTCGAACTTAT<sup>1</sup>CCGGTAAATGCAACATTGAAGC 2198

[illegible]

QY 2281 GCTGTTAACAAATAAGCGAAAAGGTTGTGAGTCCTATGTTTACAAGTAGTACGAAAA 2340 QY

2100

Db 2199 AGAAGAAGACCTAGATGTGGCAAGAAAGCAGTAAATGGCTTGTTACGAGTAAAAAGA 2258

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Db 2379 GAAACGACTGTTTCAGGACGTAACCTTACTCCAGAGATACAGGCTTTTAATAGGATTAATGG 2438  
Qy 2519 -----TGACACATCGGTAATGATATTTATCATAGATCCAATAAATCCTATTTTAA 2568  
Db 2439 AGAAACCGATGCGAGGGAATACGGGAATCGAGGTTCGGAGGAGATGTTCTGTTAA 2498  
Qy 2569 AGGAAATTTCTACAGATCGGTGAGACACAGACATATATGNACTCTATTTCCAACTTA 2628  
Db 2499 AGATCGTTCGCTTCGTTTACAAAGTCGAGAGAGATTGATACAGAAACATATCCAACTTA 2558  
Qy 2629 TATCTGCAAAATATAGATGAGTCTAAATTTAAACCATATACACGTTTATCGAGTAAGAG 2688  
Db 2559 TCTCTATCAACAATATAGATGAATCACTTTTAAACCATATACAGATATTAACATAAGG 2618  
Qy 2689 GTTGTGGGAAGTAGTAAGATTGAAATTTAAATGGAACACGTTACGGGAAGAAATGCA 2748  
Db 2619 TTTTATAGGAAGTAGTCAAGATTTAGAGATTTAAATTAATACGTCATCGGGCAATCAAAT 2678  
Qy 2749 TGCTATCATGAATGTTCCAAATGATTTGGCTATATGCAAGCTTAATCCTTCATGTGGAGA 2808  
Db 2679 CGTCAAAATATGACCAAGATTAATCTCTGCGAGATGTACTCCCTGTCAATTTCTGTGGTG 2738  
Qy 2809 TTATCGCTGGAATCATCGTCTCAGTATGTGACCAAGGTATCTTACACCAACACATGG 2868  
Db 2739 GATCGATCGCTGACGATGACGACGATATGTAGACGGAATTTAGCACTCGAAACCAATGG 2798  
Qy 2869 ATATGCTCCCGATATGATATGCAATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCA 2928  
Db 2799 AGAAATGCAATATGCTCTCT ----- 2820  
Qy 2929 CGATCGTATCCATTTGATTTTTCATATTTGACACCGGAGATAGATACAAATACAATGT 2988  
Db 2821 -GATTTCCCATGCAATTTCTTTTCCATATTTGATACAGGTGAATAGATTTGAATGAAATAC 2879  
Qy 2989 AGTATTTGATGCTTATTAATAATTTCTAATCCAGATGGATAGCTACAGTAGGGGAATCT 3048  
Db 2880 AGGAATTTGGTTCGATTTTAAATTTCCGACACAAATGATAGCAGCACTAGGAATTT 2939  
Qy 3049 AGAAGTCAATGAAGAAGGACCACTAACAGGTGAAGCATTTGGCAATGTGAAACAAAGGA 3108  
Db 2940 TGAATTTGGTAGAAGAGGGGCCATTTGTGAGGGAAACATTTAGAACGAGCACAACAAAGA 2999  
Qy 3109 AAAGRAATGGAACACACATGAGAAAGAAACCTTTGGGAAACACACCAAGCCTATCATCC 3168  
Db 3000 ACAACATGGAAGCAAAATGGAAGAAACGTTGGGCGATCAGAAAGCATATTTATGC 3059  
Qy 3169 AGCAAAACAGGCTGTAGATGCAATTTTACAAATGAACAGAGTTACATCATATATTAC 3228  
Db 3060 AGCAAGCAAGCATTTGATCGTTTATTCGAGATTTATCAAGACCAAAACTTAATTTCTGG 3119  
Qy 3229 TTTAGA-----TCATATTCAAACCGTGAATCGATCGATCGGTGATCGATTCCTTATGATA 3282  
Db 3120 TGTAGAAATGTCAGATATGTTGGCAGCCCAAAACCTTTGACAGTCCATTTCTTACGTATA 3179  
Qy 3283 CCATATTTGTTTACCGAATGCTCCAGTATGAACTATGATGTATATCAAGAGTTAAACGC 3342  
Db 3180 TAATGATGCTTACCAGAAATCCCTGGAATGAACATATACGAGTTTACAGAGTTTACAAA 3239  
Qy 3343 AGGTATCATGCAAGGTTTAAATTTATATGATGACGAAATGTCTAACAAATGGTGACTT 3402  
Db 3240 TAGACTCCAACAGCATGGAATTTGATGATCTTCGAAATGCTATACCAATGGAGATTT 3299  
Qy 3403 TACAAGGATTTACAGGATGCGCAGCAAGGAATGCGCGGTACAACAAAATGATGG 3462  
Db 3300 TCGAAATGGAATTAAGTATGGAATGCAACATCAGATGTGAATGTGCAACAACTAAGCGA 3359  
Qy 3463 AGCTTCAGTATGATTTCTATCAATTTGGAGCGGGGTATCTCAAACTTGCATCTCA 3522  
Db 3360 TACATCTGCTTGTCAATTCCAAACTGGAATTTCTCAAGTGTCACAAAATTTACAGTTCA 3419  
Qy 3523 AGATCATATGGATATGTTTACGTGTGATTGCGCAAAAGAGAGGACCTGGAAAAGGGTA 3582  
Db 3420 ACCGAATTATAGATATGTTTACGTGTCAAGCGAGAAAGAGGAGTAGGACCGGATA 3479

Qy 3583 TGTACGATGATGGATTGTAATGGAAAGCAGGAAACACTTAAGTTCACTTCTTGGCAAGA 3642  
Db 3480 TGTGATCATCCGTGATGGTGCGAATCAGACAGAAACACTCAATTTAATATATGTGATGA 3539  
Qy 3643 AG-----GATATATGACAAACACAGTAGAGGTATT 3672  
Db 3540 TGATACAGGTGTTTATCTGCTGATCAAACTAGCTATATCACAAAACACAGTGAATTCAC 3599  
Qy 3673 CCCAGAAAGTGCATCGGTACCGGATTGAAATAGGAGAAACCGAAGGTACATTTTATATAGA 3732  
Db 3600 TCCATCTACAGACGAAGTTTGGATTGACATGATGAGACCGAAGGTGATTATCAACATAGA 3659  
Qy 3733 TAGCATCCAGTTGCTTTGTATGCAAGGATA 3762  
Db 3660 AAGTGTAGAACTCGTGTTAGAAGAAGATA 3689

## RESULT 14

US-10-120-544A-19

; Sequence 19, Application US/10120544A

; Publication No. US20020182693A1

; GENERAL INFORMATION:

; APPLICANT: TANAKA, Maeo

; APPLICANT: YOKOYAMA, Tomoko

; APPLICANT: AOYAGI, Morichi

; APPLICANT: HASEGAWA, Makoto

; APPLICANT: EHARA, Gaku

; APPLICANT: KIMURA, Masaharu

; APPLICANT: NISHIHASHI, Hideji

; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and

; TITLE OF INVENTION: polynucleotide encoding the same

; FILE REFERENCE: OPI335

; CURRENT APPLICATION NUMBER: US/10/120,544A

; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: JP 2001-115754

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: JP 2001-203463

; PRIOR FILING DATE: 2001-07-04

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 4366

; TYPE: DNA

; ORGANISM: Bacillus popilliae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (224)..(4255)

US-10-120-544A-19

Query Match 5.3%; Score 318.6; DB 5; Length 4366;

Best Local Similarity 55.7%; Pred. No. 4.8e-56;

Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;

Qy 2292 AATAAGCGAAAAGGTTGTGAGTCTCTATGTTTACAGTAGTAGCAAAAATACGTTAAAAA 2351  
Db 2196 AAAAAAGCAAGGAAGCGGTGAACCATTTGTTTACAGATGGATCGAAAAAGGCGCTAAAAAG 2255  
Qy 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAACTGTATGTACAGATG 2411  
Db 2256 AAGACACAGACCCGATTTATGAGATTGATCAAGCGCCCAACGCTGGTAGTTGTTATTCGGATG 2315  
Qy 2412 AAAAAAATCCTCAGGAAAAAATAATGTTTATGGGATGAAATAAAACCTGGCAAAACAACTTA 2471  
Db 2316 ---AGTGTGGACATGATAAAATGATCCTGTTAGATGAAGTAAAAATATGCAAAACAACTCA 2372  
Qy 2472 GTCAGTCTGTAATCTACTCCAAAATGGAGACTTTTCT----- 2509  
Db 2373 GCCAAGCCCCGAATTTACTGCTCAATGGGAATTTTCGATGATCTATATTCAGCTCTCGAGA 2432  
Qy 2510 ---GGGAATGATTGGACATTCGGTAAATGATATTATCATAGGATCCAAATAATCCTATTTTTA 2567



Db 2433 AGGAGAAATCCATGGAAACCAAGTCCGAATGTTACGATCCGACAGATAAACCCGATTTTGA 2492  
Qy AAGGAAATTTCTACAGATCGTGGAGCAGGACATATATGGAC-----TCTATTTTC 2621  
Db 2493 AAGCCATTAATCTCAGTATGGCGGTGCGAAGCATATCGAGGCCACCAATGATACCTTCC 2552  
Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAAAACCATATACACGTTTATCGAG 2681  
Db 2553 CCAGTATGCTATCAAAAAATAGACGAAGCCAAATTTAAAGCCGTATACACGTTATTAAG 2612  
Qy 2682 TAAGAGGGTTGTGGGAGTAGTAAGATTGAAATTTAAATGTTAAACAGCTTACGGGAAAG 2741  
Db 2613 TGGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTGGTTTACACGCTATAATGAAG 2672  
Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTGGCCTATATGCGACCTTAATCCTTCAT 2801  
Db 2673 AAGTTGATGCTTTAGATGTAACGGATTAATATCCGCAATGCGCCGACTCTGTCTGCG 2732  
Qy 2802 GTGGAGATTATCGTGTGAATCATCGTCTCAGT-----ATCCTCCCG 2879  
Db 2733 GTGAATTTGATCGATGCAAGCCCTATTGCTATCCACCTTTACTTCCAGATGTAACCCCTG 2792  
Qy 2835 -----ATGTGAGCCAGGGTATCTTACACCAACAGATGGAT----- 2870  
Db 2793 AGTTTAAATCAGATGCAACCATCTCTTTGCCACCACCAATCAGATGGTCAATTAACAATA 2852  
Qy 2871 -----ATCCTCCCG 2879  
Db 2853 ACATGAACACGACGACGAGTACTACCATGTAATCTCTAGCATGAATCTCCCTTACGCGCTG 2912  
Qy 2880 ATATGATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGATCGTCATC 2939  
Db 2913 AAATAGCATCCAGCAAGTGGATTCCGCAGAAACATCGCAATGTCTCAAGCGCATC 2972  
Qy 2940 CATTTGATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGATAGGTATTGATG 2999  
Db 2973 AATTTGAGTTCCACATTTGATGATACCGGACAAATCGATTGTCGAAGATTTGGGCATTTGGG 3032  
Qy 3000 TCTTTTAAAAATTTCTTAATCCAGATGGATACCTACAGTACAGTACAGTACAGTACAGTACAGT 3059  
Db 3033 TGATCTTCAAAATCTGTGCCACAGATGGATACCAAGCTTAGATGATCTGGAAGTGAATG 3092  
Qy 3060 AAGAAGGACCACTAACAGAGTGAAGCATTTGGCAGATGTGAACCAAAAGGAAAGAAATGGA 3119  
Db 3093 AAGAAGGAGCGTGGGTGTCGAAGCATTAAGACTTGTCAAAAAGAGAAAGAAATGGA 3152  
Qy 3120 AACAAACATCGGAGAAAAAGTGGGAAACACAAAGCCTATGATCCAGCAAAACAGG 3179  
Db 3153 GACATCAGAGGAGCAGCACTGTTCCGAAACGAAACACAAATATGATGCGGCCAAACATG 3212  
Qy 3180 CTGTAGATGCATTTTACAAATGAAC-----AAGAGTTACACTATCATATTTACTTTAG 3233  
Db 3213 CGGTGATGGGTTTATTTACAAACAGCGCTATGAAAATTTGAAGTTTGAACCAACCATTT 3272  
Qy 3234 ATCATATTCAAAACGCTGATCGACTGGTACAGTTCGATTCCTATGTATACCAATATGGT 3293  
Db 3273 CTGACATTTGTATGCTGATCATCTCGTGCAGTCTGATTCCTATGTATATTAATATG 3332  
Qy 3294 TACCGAATGCTCCAGGTATGAATCTATGATGATATCAAGAGTTTAAACGACGATCATGC 3353  
Db 3333 TACCGAAGTTCCAGGTATGAATTTAGCAACTCTATTACAGAGCTTAAACACACTGGTTTACA 3392  
Qy 3354 AAGGTTATATTTATATGATGACGAAGTGTATACAAATGCTGATGCTTTTACACAGGAT 3413  
Db 3393 ATCGGTTCTACCTGTATGACCGGAATCTGATTAATAATGGCGCTTTAGCAATGGGC 3452  
Qy 3414 TACAGGGATGGCAGCAACAGGAAATGCCCGGTACAAACAAATGGAGTTCAGTAT 3473  
Db 3453 TTATGATTTGGCAAGCTACTCTCATGCAAGATAGCAAGATATGAGAAATCGGTGC 3512  
Qy 3474 TAGTTCTATCAAAATTTGAGCGGGGGTATCTCAAAATTTGCAATTTGCAAGTATCATCATG 3533  
Db 3513 TCGTGTGCAAAATTTGGGATGCCAATGTGTGCGAAGATCTTTGTATCGAACAACAAATCGCG 3572

Qy 3534 GATATGTTTACGTTGATTTGCCAAAAAGAGGACCTCGAAAAAGGTATGTACAGATGA 3593  
Db 3573 GTTATGTTTTCGCTGTACCGCGAGAAAAAGATCGGGAGCTGGCAATGTGTACCTTTA 3632  
Qy 3594 TGGATTGTAATGAAAGCAGGAAACACTTAAAGTTTCACTTCTTCGGAAGAG 3644  
Db 3633 GTCACTGTGAAATCATGTGCAAGCTGAGCTTTACTTCTTGGGATATAG 3683

## RESULT 15

US-11-091-654-19  
; Sequence 19, Application US/11091654  
; Publication No. US20050172355A1  
; GENERAL INFORMATION:  
; APPLICANT: TANAKA, Masao  
; APPLICANT: YOKOYAMA, Tomoko  
; APPLICANT: AOYAGI, Morichi  
; APPLICANT: HASEGAWA, Makoto  
; APPLICANT: EHARA, Gaku  
; APPLICANT: KIMURA, Masaharu  
; APPLICANT: NISHIHASHI, Hideji  
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
; TITLE OF INVENTION: polynucleotide encoding the same  
; FILE REFERENCE: OP1335  
; CURRENT APPLICATION NUMBER: US/11/091,654  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: JP 2001-115754  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: JP 2001-203463  
; PRIOR FILING DATE: 2001-07-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 4366  
; TYPE: DNA  
; ORGANISM: Bacillus popilliae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (224)..(4255)  
US-11-091-654-19

Query Match 5.3%; Score 318.6; DB 10; Length 4366;  
Best Local Similarity 55.7%; Pred. No. 4.8e-56;  
Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;

Qy 2292 AATAAGCGAAAAAGGTTGTAGTCTCTTACAGTAGTACGAAAAATACGTTAAAAA 2351  
Db 2196 AAAAGCAAGGAAAGCGGTGAACCATTTGTTTACAGATCGATCGAAAAAGGCGCTAAAG 2255  
Qy 2352 TGAACACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGTATGTCAGATG 2411  
Db 2256 AAGACACGACCGATTATGAGATTGATCAAGCGCCCAACGTTGATATCGATG 2315  
Qy 2412 AACAAAATCCTCAGGAAAAATATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471  
Db 2316 ---AGTGTGGACATGATAAAATGATCCTGTTAGATGAAGTAAATATGCAAAACAACTCA 2372  
Qy 2472 GTCACTCTCGTAACTTACTTCCAAAAATGGAGACTTTTCT----- 2509  
Db 2373 GCCAGCCGCAATTTACTGCTCAATGGAAATTCGATGATCTATATTTCAGTCTCGAGA 2432  
Qy 2510 ---GGGAATGATTGGACATTTCCGTAATGATATTTATCATAGAGTCCAAATATCTTATTTTA 2567  
Db 2433 AGGAGAAATCCATGGAAAAACAAGTCCGAATGTTACGATCCGACAAAGATAACCCGATTTTGA 2492  
Qy 2568 AAGGAAAAATTTCTACAGATGCGTGGACGACGACATATATGGAAC-----TCTATTTC 2621  
Db 2493 AAGGCCATTATCTCAGTATGGCGGGTGGCAACGATATCGAGGCCCACTATGATACCTTCC 2552  
Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTTAAATTTAAAAACCATATACACGTTATCGAG 2681

Db 2553 CCACGTATGCTCTATCAAAAATAGACGAAGCCAAATTAAGCCGTATACACGTTATAAAG 2612  
Qy 2682 TAAGAGGGTTGTGGGAAGTAGTAAAGATTGAAATTAATGGTAACACGTTACGGGAAAG 2741  
Db 2613 TCGCGGGTTGTGGCAGCAGCAAGCTCTAGAGCTGTGGTTACACGCTATATGAAG 2672  
Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATGACAGCCTAATCCTTCAT 2801  
Db 2673 AAGTTGATCGATTTTAGATGTACCGGATAATATCCGCATGCGCGGACTCTCTGTCTGCG 2732  
Qy 2802 GTGGAGATTATCGCTGTAATCATCTCTCAGT----- 2834  
Db 2733 GTGAATTTGATCGATCGAAGCCCTATTTCGTATCCACTTTACTTCAGAAATGTAAACCCTG 2792  
Qy 2835 -----ATGTGAGCCAGGGTATCCTACACCAACAGATGGAT----- 2870  
Db 2793 AGTTTATAAATCAGATGCAACCCTCTCTGCCACCACCAATCAGATGGTTCGATTACAATA 2852  
Qy 2871 -----ATGCTCCCG 2879  
Db 2853 ACATGAACACGACGACGAGTACTACCATGAATCCTAGCATGAATCCTCCCTTACGCCCTG 2912  
Qy 2880 ATATGTAATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACGATCGTCATC 2939  
Db 2913 AAATAGCATCCAGCCAAAGTGGAATCGGCAGAAAACATCGCAAAATGTCTCAAGCGCATC 2972  
Qy 2940 CATTTGATTTTCATATTGACCCGGAGAAAGTAGATACAAATACAAATGTAGGTATTGTG 2999  
Db 2973 AATTTGAGTTCCACATTTGATACCGGGACAATCGATTTGGTCGAAGATTTGGGCAATTTGGG 3032  
Qy 3000 TCTTATAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAAAGTCATTG 3059  
Db 3033 TGAATCTTCAAAATCTGTGCCACAGATGGATACGCAAGCTTAGATGATCTGGAAGTGATTG 3092  
Qy 3060 AAGAAGGACCACTAACAGGTGAAGCATTGGCAGATGTGCAATGTGAACAAAGAAAGAAATGGA 3119  
Db 3093 AAGAAGGAGCGCTGGGTGCGAAGCAATAGAACTTGTCAAAAAGAGAAAGAAATGGA 3152  
Qy 3120 AACAAACATGGAGAAAAACGTTGGGAAACACAACAGCCTATGATCCAGCAAAACAGG 3179  
Db 3153 GACATCAGAAGGAGCAGCACTGTTCCMAACGAAACACAATATGATCGGCCCAACATG 3212  
Qy 3180 CTGTAGATGCATTTTACAATGAAC-----AAGAGTTACACTATCATTTACTTTAG 3233  
Db 3213 CGGTGATGCGGTTATTACAAACAGCGCTATGAAAAATTGAAGTTTCGAAAACAACCATTT 3272  
Qy 3234 ATCATATTCAAAACGCTGATCGACTGCTACAGTCGATTCCTATGTAATACCATTAATTGTT 3293  
Db 3273 CTGACATTTTGTATGCTGATCATCTCTGTCAGTCGATTCCTTATGTAATATAAATATG 3332  
Qy 3294 TACCGAATGCTCCAGGTATGAATCATGATGTATATCAAGAGTTAAACGACGCTATCATGC 3353  
Db 3333 TACCGGAAGTCCAGGTATGAATTTACGAACTCTATTACAGAGCTAAACACACTGGTTTCAGA 3392  
Qy 3354 AAGGTTATATTTATATATGATGACGAAATGTCTATAAATGGTGAATTTTACACAGGAT 3413  
Db 3393 ATGCGTTCTACCTGTATGATCCAGCGGAATCTGATTAAAAATGGGCGCTTTAGCAATGGGC 3452  
Qy 3414 TACAGGGATGGCAGCAACAGGAAATGCCGCGTACAAACAAATGGATGGAGCTTCAGATAT 3473  
Db 3453 TTATGCATTTGGCAGGCTACTCCTCATGCAAGATAGAGCAAGNATATGAAATCGGTGC 3512  
Qy 3474 TAGTTCTATCAATTCGAGCGGGGGTATCTCAAACTTGCATGCTCAAGATCATCATG 3533  
Db 3513 TCGTGTGCCAAATTTGGGATGCCAATGTGTGCAAGATCTTTGTATCGAACAACATCGCG 3572  
Qy 3534 GATATGTTTACGTGTGATTTGCCAAAAGAGAGCACTCGGAAAAGGGTATGTAAAGCATGA 3593  
Db 3573 GTTATGATTTGGGTGTCTACGGCGAGAAAAGAGATCCGGGAGCTGGCAATGTTTACCTTTA 3632  
Qy 3594 TGGATTGTAATGGAAAGCAGGAAACACTTAAGTTTCACTTCTTCTCGGAAGAG 3644  
Db 3633 GTGACTGTGAAATCATGTGCAAGCTGAGCTTTACTTCTTTCGGATATAG 3683



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Db      2440  ---AGTGTGGACATGAGAAATGATCTGTGTTAGATGAAGTAAATAATGCAAAACCACTCA 2496
QY      2472  GTCAAGTCTGTAATCTACTTCCAAATGGAGACTTTTCT-----2509
Db      2497  GCGAGCCGCAATTTACTGCTCAATGGGAATTCGATGATCTATATCAGCTCTGGAGA 2556
QY      2510  --GGGAATGATTGGACATTTGGTAAATGATATTATCATAGGATCCAATAATCTCTATTTTA 2567
Db      2557  GGGAGAATCCATGGAAAAAAGTCCGCGATGTTACGATCCGTCAAGATAACCCGATTTTA 2616
QY      2568  AAGGAAATTTCTACAGATGCGTGGAGACGAGACATATATGGAAC-----TCTATTTC 2621
Db      2617  AAGGCCATTATCTCAGTATGGGGGTGCGAAGCATATGAGGCCACCAATGATACCTCC 2676
QY      2622  CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTAATAACCATATACACGTTATCGAG 2681
Db      2677  CACGATGATCTATCAAAAATAGACGAGCCAAATTAAGCCATATACACGGTATAAG 2736
QY      2682  TAAGAGGGTTTGTGGGAAGTAGTAAAGATTGGAATTAATGGTAAACAGCTTACGGGAAAG 2741
Db      2737  TGGCGGGTTTGTGTAGCAGCAAGCTCTAGAGCTGTGGTTACACGCTATAATGAAG 2796
QY      2742  AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCCTATATGAGCCCTAATCTTCA 2801
Db      2797  AAGTCGATCGATTTTGTAGATGTACCGGATAATATCCGCGATGCGCGACTCTCTGTGCG 2856
QY      2802  GTGGAGATTATCCCTGTGAATCATCTGC-----TCAGTATGTGAGCCAAG 2846
Db      2857  GTGAATTTGATCGATCGAAGCCCTATTTGATATCCACTTTACTTCCAGATGTAAACCTG 2916
QY      2847  GGTATCCTACACAAACAGATGGATATGCTCCGATATGATGCATGCCGCGCAAAATATAG 2906
Db      2917  AGTTTATAATCAGATGCAACCATCTCTTGCCACCAATCAGATGGTGGATTAATA 2976
QY      2907  ATAGAAGATGTGAAGTGTACGATCGTCAATCCATTTGATTTTATATGACACGGAG 2966
Db      2977  ACAGAAAACACCGCAATGTTCATCAAGCGCATCAATTTGAGTTCCATATTTGATACCGGA 3036
QY      2967  AAGTAGATACAAATGATGATGATGCTTTATTAATAAATTTCTAATCCAGATG 3026
Db      3037  CAATCGATCTGGTGAAGATTTGGGCAATTTGGGTGATCTTCAAAATCTGTGCCACAGATG 3096
QY      3027  GATACGCTCAGTAGGGAATCTAGAAGTATTGAAGAAGCACTAACAGGTGAAGCAT 3086
Db      3097  GTTACGCAAGCTTAGATGATTTGGAAGTATTGAAGAAGGAGCGCTGGGTGTGGAAGCAT 3156
QY      3087  TGGCAGATGTGAACAAAGGAAGAAATGGGAACAAACATATGGGAAGAAACGTTGGG 3146
Db      3157  TAGAATTTGTCAAGAAAAGAGAAAAGAAATGGAGACATCAGAAAGGAGCGACTGTGTCG 3216
QY      3147  AAACACAAAGCCTATGATCCAGCAAAACAGGCTGTAGATGATTAATTTACAAA----- 3201
Db      3217  AAACGAAACAAATATGATCGGCCAAACACGCGGTGATGGGTTATTTCACAAACACGC 3276
QY      3202  -TGAAACAGAGTTACATACTATATTAATTTAGATCATATTTCAAAACGCTGATCGACTGG 3260
Db      3277  GCTATGAAAAATTTGAAGTTTGAACCAACCATCTCCAATATTTTGTATGTGATCATCTCG 3336
QY      3261  TACAGTCGATTCCTATGATATACCAATATTTGGTACGGATGCTCCAGGTATGAACTATG 3320
Db      3337  TGCAATGATTCCTATGATATATAAATATATATATGATCCGGAAGTTCCAGGTATGAAATACG 3396
QY      3321  ATGTATATCAAGAGTTTAAACGACGCTATCATGCAAGTTTATATTTATATGATGACAGAA 3380
Db      3397  AACTCTATACAGAGCTAAACACTCTGTTCCAGATGGGTTCTATCTATATGACCGGGA 3456
QY      3381  ATGTCTATAAATAATGTTGACTTTTACAAAGATTAACGGATGGCAGCAACAGGAAATG 3440
Db      3457  ATCTGATTAATAATGGCGCTTTTAGCAATGGGCTTATGATTTGGAGGGCTACCCCGCATG 3516
QY      3441  CCGCGGTACAAACAAATGGATGGAGCTTCAGTATTTAGTTTCTATCAAAATTCGAGCGCGGG 3500
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Db      3517  CACGAGTGGAAACAAGAATATGAGAAATCTGTACTCGTCTGCCAAATTTGGGATGCCAATG 3576
QY      3501  TATCTCAAAACTTGCATGCTCAAGATCATATGATATGTTTACGTTGATTTGCCAAAA 3560
Db      3577  TGTCCAGAGATCTTTGTATCGACACAATCGGGTTATGTTGCGTGTCACGGCGAGA 3636
QY      3561  AAGAAGGACCTGGAAAGGGTATGTAAAGATGATCGATGATGATGTAATGGAAGCAGGAACAC 3620
Db      3637  AAGAAGATCCGGAGCTGGCAATGTACCTTCAGTGAATGTGCAAAACCATGTGCAACAGC 3696
QY      3621  TTAAGTTTCACTTCTTTCGCAAGAG 3644
Db      3697  TGAGCTTACTTCTTTCGCGATATAG 3720
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## RESULT 2

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US-11-091-643-19
; Sequence 19, Application US/11091643
; Publication NO. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: Insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4366
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)..(4255)
US-11-091-643-19
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Query Match 5.3%; Score 318.6; DB 9; Length 4366;  
Best Local Similarity 55.7%; Pred. No. 3.8e-58;  
Matches 831; Conservative 0; Mismatches 519; Indels 141; Gaps 6;

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QY      2292  AATAAGCGAAAAGTTGTGAGTCTCTATGTTTACAAAGTAGTACGAAAAATACGTTAAAAA 2351
Db      2196  AAAAAGCAAGAAAGCGGTGAACCAATTTGTTTACAGATGATCGAAAAAGCGCTTAAAG 2255
QY      2352  TAGAAAACGACAGATTATGAATATAGATCAAGCGGCCATTTTCTATAGAAATGATGTAGATG 2411
Db      2256  AAGACACGACCGATTATGAGATTGATCAAGCGCCAAACGCTGTAGATTGTTATATCGATG 2315
QY      2412  AACAAAATCCTCAGAAAAAATAATGTTATGGGATGAATAAATAAACTGGCAAAACAACTTA 2471
Db      2316  ---AGTGTGGACATGATAAATGATCTCTGTTAGATGAAGTAAATATGCAAAACAACTCA 2372
QY      2472  GTCAAGTCTGTAATCTACTCCAAAATGGAGACTTTTCT-----2509
Db      2373  GCCAAGCCGCAATTTACTGCTCAATGGGAATTCGATGATCTATATTCAGCTCTGGAGA 2432
QY      2510  --GGGAATGATTGGACATTTCCGTAATGATATTTATCATAGGATCCAATAATCTCTATTTTA 2567
Db      2433  AGGAGAAATCCATGGAAAAACAAAGTCCGAATGTTACGATCCGACCAAGATAACCCGATTTTA 2492
QY      2568  AAGGAAAATTTCTACAGATGCGTGGAGCAGACATATATATGGAAC-----TCTATTTC 2621
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Db 2493 AAGGCCATTATCTCAGTATGGCGGTGCGAACGATATCGAGGCCACCAGTATGATACCTTCC 2552  
QY 2622 CAACCTATATCTGTCACAAAATAGATGAGTCTAAATTTAAACCATATACACGTTATCGAG 2681  
Db 2553 CCACGATGCTATCAAAAATAGACGAGCCAAATTTAAAGCCGATATACACGTTATAAG 2612  
QY 2682 TAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTTAAATGTTAAACACGTTACGGGAAAG 2741  
Db 2613 TGGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTGGTTTACAGGCTATAATGAAG 2672  
QY 2742 AAATTGATGATCATGATGTTCCAAATGATTTGGCCTATATGCGCCCTAAATCCTTCAT 2801  
Db 2673 AAGTTGATGCGATTTAGATGTACCGGATTAATATCCGCAATATGCGCCGACTCTCTGTCTGCG 2732  
QY 2802 GTCGAGATTAATCGTGTGAATCATCTGCTCAGT----- 2834  
Db 2733 GTGAATTTGATGATGCAAGCCCTATTCTGATATCAACCTTTTCCAGAAATGAACCCCTG 2792  
QY 2835 -----ATGTGAGCCAAAGGGTATCTCTACACCAACAGATGGAT----- 2870  
Db 2793 AGTTTATAATCAGATGCAACCATCTCTTGGCCACCAATCAGATGGTCTGATTACANTA 2852  
QY 2871 -----ATGCTCCCG 2879  
Db 2853 ACATGAACAGCAGCAGGAGTACTACCATGAATCTTAGCATGAATCTCTCCCTTTACGCCCTG 2912  
QY 2880 ATATGATGATGATGCGCGCAAAATATAGATAGAAGCATGTGAAGTGTACGATCGTCATC 2939  
Db 2913 AAATAGCATCCAGCCAAAGTGGATTCGGCAGAAAACATCGCAATGTCTCAAGCCGATC 2972  
QY 2940 CATTTGATTTTCATATTTGACACCGGAGAGTAGATACAAATGATAGTATTGATG 2999  
Db 2973 AATTTGAGTTCCATTTGATACCGGACATCATCTTTGGTGAAGATTTGGGCAATTTGGG 3032  
QY 3000 TCTTATTAATAATTTCTAATCTCAGATGGATACGCTACAGTGAAGATCTAGAAAGTCAATG 3059  
Db 3033 TGATCTTCAAAATCTGTGCCACAGATGGATACCAAGCTTAGATGATCTGGAAGTGAATG 3092  
QY 3060 AAGAAGGCCACTAAACAGGTGAAGCATTCGCATGTGAACAAAGAAAGAAAGAAATGGA 3119  
Db 3093 AAGAAGGCGCTGGGTGTGGAAGCATTAAGATTTGTCAAAAAGAGAAAGAAATGGA 3152  
QY 3120 AACACACATGGAGAAAAACGTTGGAAACACAAAGCCTATGATCCAGCAAAACAGG 3179  
Db 3153 GACATCAGAAGGAGCAGCTGTTCCGAAACGAAACACAAATATGATGGCGCAACATG 3212  
QY 3180 CTGTAGATGATTTTACAAATGAAC-----AAGAGTTACACTATCATATTACTTTAG 3233  
Db 3213 CGGTGATGGCTTATTTTACAAACAGCGCTATCGAAAAATTTGAAGTTTCAAAACCACTTT 3272  
QY 3234 ATCATATTTCAAAACGCTGATCGACTGGTACAGTTCGATTCCTATGTATACCATTAATGGT 3293  
Db 3273 CTGACATTTTGTATGCTGATCATCTCGTGAAGTCGATTCCTTATGTATTAATAATATG 3332  
QY 3294 TACCGAATGCTCCAGGTATGAACATATGATGTATATCAAGATTTAAACGACGATCATATG 3353  
Db 3333 TACCGAAGTTTCAGGTATGAATTAAGAACTTATTCAGAGCTTAACACACTGGTTTCA 3392  
QY 3354 AAGGTTTAAATTTATGATGACGAAATGTCTATAAATAATGGTGACTTTTACACAAAGGAT 3413  
Db 3393 ATGCGTTTCTACCTGTATGACAGCGAAATCTGATTTAAATAATGGCGCTTTAGCAATGGG 3452  
QY 3414 TACAGGATGGCAGCAACAGGAAATGCGCGGTACAAATAATGGATGGAGCTTCAGTAT 3473  
Db 3453 TTAATGATTTGGCAAGCTATCTCTCATGCAAGATAGAGCAAGAAATATGAGAAATCGGTG 3512  
QY 3474 TAGTTCTTCAAAATTTGGAGCGCGGTATCTCAAAATTTGCAATGCTCAAGATCATCATG 3533  
Db 3513 TCGTGTGCAAAATTTGGGATGCCAATGTGTGCGAAGATCTTTGTATCGAACCAATCGCG 3572  
QY 3534 GATATGTTGATGATTTGCCAAAAAAGAGGACCTTGGAAAGGGTATGTAAACGATGA 3593

Db 3573 GTTATGTTATGCGTGTACGGCGAGAAAAAGAGATCCGGAGCTGGCAATGTTTACCTTTA 3632  
QY 3594 TGAATGTTATGAAAGCAGGAAACACTTAAAGTTTCACTTCTTTCGGAAGAAG 3644  
Db 3633 GTGACTGTGAAATCATGTGACAAAGCTGAGCTTTACTTCTTCGATATAG 3683  
RESULT 3  
US-11-091-643-17  
; Sequence 17, Application US/11091643  
; Publication No. US20050246789A1  
; GENERAL INFORMATION:  
; APPLICANT: TANAKA, Masao  
; APPLICANT: YOKOYAMA, Tomoko  
; APPLICANT: AOYAGI, Morichi  
; APPLICANT: HASEGAWA, Makoto  
; APPLICANT: EHARA, Gaku  
; APPLICANT: KIMURA, Masaharu  
; APPLICANT: NISHIHASHI, Hideji  
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
; TITLE OF INVENTION: polynucleotide encoding the same  
; FILE REFERENCE: OP1335  
; CURRENT APPLICATION NUMBER: US/11/091,643  
; CURRENT FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: JP 2001-115754  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: JP 2001-203463  
; PRIOR FILING DATE: 2001-07-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 4359  
; TYPE: DNA  
; ORGANISM: Bacillus popilliae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (250)..(4245)  
US-11-091-643-17  
Query Match 5.2%; Score 312.2; DB 9; Length 4359;  
Best Local Similarity 55.5%; Pred. No. 8.6e-57;  
Matches 827; Conservative 0; Mismatches 523; Indels 141; Gaps 6;  
QY 2292 AATNAGCGAAAAAGTTGTGAGTCTCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA 2351  
Db 2186 AAAAAAGCAAGAAAGCGGTGAACCAATTTGTTTACAGATGGATCGAAAAAGGCGCTAAAG 2245  
QY 2352 TAGAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGTATGTCAGATG 2411  
Db 2246 AAGACAGACCGATTTATGAGATTGATCAAGCGCCACCGGATGTTGTTATATCGATG 2305  
QY 2412 AACAAAAATCCTCAGGAAAAAATAATGTTATGCGATGAAATAAAACCTGGCAAAACAACCTTA 2471  
Db 2306 ---AGTGTGGACATGAGAAAAATGATCTCTGTAGTGAAGTAAAAATATGCAAAACAACCTCA 2362  
QY 2472 GTGAGTCTGTTAATCTACTCCAAAATGGAGACTTTTCT----- 2509  
Db 2363 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTTTCGATGATCTATATCCAGCTCTCGAGA 2422  
QY 2510 ---GGGAATGTTGGACATTCGGTAAATGATATTATCATAGGATCCCAATAATCCTATTTTTA 2567  
Db 2423 GGGAGATCCATGGAAAAACAGTCCGAATGTTTACGATCCGTCAAGATAAACCCGATTTTTA 2482  
QY 2568 AAGGAAAAATTTCTACAGATGCGTGGGACGACGACATATATGGAAC-----TCTATTTC 2621  
Db 2483 AAGGCCATTATCTCAGTATGGCGGTGCGAACGATATCGAGCCACCAATGATACGTTCC 2542  
QY 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAAAACATATACACGTTATCGAG 2681  
Db 2543 CCACGATGCTCTATCAAAAAATAGATGAAGCCCAATTTAAAGCCATATATACACGTTATAAG 2602  
QY 2682 TAAGAGGGTTTGTGGGAAGTAGTAAAGATTTGAAATTAATGTTAACACAGCTTACGGGAAG 2741

[illegible]

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US-11-091-643-5
; Sequence 5, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; insecticidal effect on scarabaeidae insects and
; FILE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OP1335
; CURRENT APPLICATION NUMBER: US/11/091,643
; PRIOR FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4188
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4158)
US-11-091-643-5

Query Match          5.2%   Score 308.2;   DB 9;   Length 4188;
Best Local Similarity 55.2%;   Pred. No. 6e-56;
Matches 81;   Conservative 0;   Mismatches 533;   Indels 129;   Gaps 6;

Qy 2292 AATAAGCGAAAAAGTTGTGAGTCCTATGTTTACAAGTAGTACGAAATAACGTTAAAAA 2351
Db 2066 AAAAAGCAAGAAAGCGGTGAACCATTTGTTTACAGATGCGATCGAAAAAGCGCTAAAG 2125

Qy 2352 TAGAAACGACAGATTATGAATAGATCAAGGGCCATTTCTATAGATGTTATGTCAGATG 2411
Db 2126 AAGCGACGACAGATTATGAGATCGATCAAGCCGCCAACGGTGGATGTTATATCGGATG 2185

Qy 2412 AACAAAAATCCTCAGAAAAATAATGTTATGGGATGAAATAAAACTGGCAAAACCACTTA 2471
Db 2186 ---AGTGTGACATGAGAAATGATCCTGTGTGATGAGTGAATGCAATATGCAAAACACTCA 2242

Qy 2472 GTCAGTCTCGTAATCTACTCCAAATGGAGACTTTTCT----- 2509
Db 2243 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTTGCGATGATCTATATCCAGCTCTGGAGA 2302

Qy 2510 --GGGAATGATGGACATTCGGTAATGATATTATCATAGATCCAATAATCCTATTTTAA 2567
Db 2303 GGGAGAAATCCATGGAAAAACAAGCCCGAATGTTACGATCCGTCAAGATAACCCGATTTTAA 2362

Qy 2568 AAGGAAATTTCTACAGATCGGTGGACGACGACATATATGGAAC-----TCTATTTC 2621
Db 2363 AAGGCCAATATCTCAGTATGGCGGTGCGAACGATATCGAGGCCACCAATGATACCTTCC 2422

Qy 2622 CAACCTATATCTGTCAAAAAATAGATGAGTCTAAATTTAAAAACCATATACACGTTTATCGAG 2681
Db 2423 CCACGTATGCTATCAAAAAATAGACGAAGCCAAATTTAAAGCCGATATACACGTTTATAAG 2482

Qy 2682 TAAGAGGGTTTGTGGGAAGTAGTAAAGATTGAAATTAATGTTAAACAGTTACGGGAAG 2741
Db 2483 TGC CGGGTTGTTGGCAGCAGCAAAAGCTCTAGAGCTGTTGGTTTACACGCTATAATGAAG 2542

Qy 2742 AAATTGATGCTATCATGAATGTTCCAAATGATTTGGCCTATATATGCGACCTAAATCCTTCAT 2801
Db 2543 AAGTCGATGCGATTTTATAGTGTACCGGATTAATATCCCGATGCGCCGATACCTGCTCGCG 2602

Qy 2802 GTGAGATTTATCGCTGTGAATCATCGTC-----TCAGTATGTGAGCCAA 2845

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Db 2603 GTGAATTTGATCGATGAAGCCCTATTTCGTATCCACCTTTACTTCCAGAAATGAACCCCTG 2662
Qy 2846 GGGTA-----
Db 2663 AGTTTAAATCAGATCAACCAATCCCTCTTGGCCACCACTCAGATGGTGCATTACAATA 2722
Qy 2851 -----TCTTACCAACACAGATGGATATGCTCCCGATATGTATGCAT 2891
Db 2723 ACATGAACATGAGCAGCAGTACTACCATGAATCCTACCCCTACCGCTGAATAGCATCCA 2782
Qy 2892 GCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACAGTGTCAAGTGTCTCATTCATTTGATTTTC 2951
Db 2783 GCCAAAGTGGATTCCGGCAGAAAACATCGCAATGTCTCAAGCGCATCAATTTGAGTTCC 2842
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Qy 3012 TTTCTAATCCAGATGGATAGCTACAGTAGGGAATCTAGAAAGTCAATTGAAGAAGGACCA 3071
Db 2903 TCTGTGCCACAGATGGTTACGCAAGCTTAGATGATTTGGAAGTCAATTGAAGAAGGAGCGC 2962
Qy 3072 TAACAGGTGAAGCATTTGGCAATGTGAAACAAAGGAAAGAAATGGAACAAACATGCG 3131
Db 2963 TGGGTGTGCAAGCATTTAGAACTTTGTCAAGAAAGAGAAAGAAATGGAGACATCAGAAG 3022
Qy 3132 AGAAAAACCTTGGGAACACACACAGCTTATGATCCAGCAACACAGCTGTAGATGCAT 3191
Db 3023 AGCAGCACTTTCCGCAACCAACCAAAATATGATGCGGCCCAACATGCGGTGATGCGCGT 3082
Qy 3192 TATTTCACAA-----TGAACAAGAGTTACATCATATATTTAGATCATATTCAAA 3245
Db 3083 TATTTCACAAACCGCGTATGAAATTTGAAGTTCGAAACCAACATTTCTGACATTTTGT 3142
Qy 3246 ACCTGTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3305
Db 3143 ATGCTGATCATCTCGTGCAGTCGATCCCTTATGATATATATAAATATGATGATGATGAT 3202
Qy 3306 CAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3365
Db 3203 CAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3262
Qy 3366 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3425
Db 3263 TGATGACAGCGGATCTGATTAATAATGCGCGCTTTAGCAATGGCTTATGATGATGATG 3322
Qy 3426 ACGCAACAGGAATGCGCGGTACAAACATGATGATGATGATGATGATGATGATGATGATGAT 3485
Db 3323 AAGCTACTCTCATGCAAGAGTAGAGCAAGAAATGAGAAATCGGTCTGCTGCTGCCAA 3382
Qy 3486 ATTGGAGCGCGGGTATCTCAAACTTGCATGCTCAAGATCATGATGATGATGATGATGATG 3545
Db 3383 ATTGGAGTCCAATGTGTCGAAGATCTTTGATGCAACCAATTCGGGTATGATGATGATG 3442
Qy 3546 GTGTGATTTGCCAAAAAGAGGACCTTGAAGAGGATGATGATGATGATGATGATGATGATGAT 3605
Db 3443 GTGTCAAGCGGAGAAAGAGATCCGGGAGCGGCAATGTTACTTTAGTGACTGTGCCAA 3502
Qy 3606 GAAAGCAGGAAACACTTAAGTTCACTTCTTGGCAAGAA 3644
Db 3503 ATCATGTCAACAGCTGAGCTTTACTTCTTGGCATATAG 3541
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RESULT 5  
US-11-058-727-1  
; Sequence 1, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn

```
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3621  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3621)  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Cry1218-1  
; US-11-058-727-1
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Query Match 5.1%; Score 307; DB 7; Length 3621;  
Best Local Similarity 55.7%; Pred. No. 1e-55;  
Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;  
  
Qy 2292 AATAAGCGAAAAAGGTTGTGAGTCCCTATGTTTACAAAGTAGTAGTACGAAAAATACGTTAAAAA 2351  
Db 2018 AAGCAGCGAAGAAAGCAGTGAATGCCCTGTTTAC---GAATACAAAAGATGGCTTAGCAC 2074  
Qy 2352 TAGAAACGACAGATTTATGAATAGATCAAGCGGCCATTTCTATAGAAATGATGTCAGATG 2411  
Db 2075 CAGGCGTAACGGATTTATGAATGAATCAAGCGGCAAACTTAGTGAATGCTTATCGGATG 2134  
Qy 2412 AACAAAATCCTCAGGAAAAATAATGTTATGGATGAAATAACTGGCAAAACAACTTA 2471  
Db 2135 ATTTGATCCAAATGAAAACCGATTTGTTATTTGATGAGTAGAGAGGCAAAACGGCTCA 2194  
Qy 2472 GTCAGTCTCGTAATCTACTCCAAAAATGGAGACTT-----TTCTGGGAATGATT 2519  
Db 2195 GTGAGCAGCTAATTTGCTTCAAGATCCAGATTTCCAAGAGATAAATGGAGAAATGGCT 2254  
Qy 2520 GGCATTCGGTAAATGATATATCATAGGATCCAAATATCCTATTTTAAAGGAAAATTTTC 2579  
Db 2255 GGACGGCAAGTCCGGGAATTTAGGTTATAGAAAGGGGATGCTTTATTTCAAAGGCGTTATC 2314  
Qy 2580 TACAGATGCTGAGCAGCAGACATATATGGAACCTATTTCCAACTTATCTGTCATA 2639  
Db 2315 TAGCCCTACAGGTCCGAGAGAAATAGATACGGAACGATTCACAGATCTCTGTATCAAA 2374  
Qy 2640 AAATAGATGAGTCTAAATTTAAACCAATATACAGCTTATCGAGTAAGAGGTTTGTGGAA 2699  
Db 2375 AAGTAGAGGAAGTGTATTAAACCATACACAAGATATAGATTGAGAGGTTTGTTCGAA 2434  
Qy 2700 GTAGTAAGATTTGAAATTAATGTTAACACGTTTACCGGGAAGAAATGATGCTATCATGA 2759  
Db 2435 GCAGTCAAGGATTTGGAATTTTTCACAAATTCGTCA-----TCAACCAACCGAA 2482  
Qy 2760 ATGTTCCAAATGATTTGGCCTATATGACGCTTAATCCTTTCATGTCGAGATTTATCGCTG 2819  
Db 2483 TTGTAATAAATGATGACCGGATGATTTGCTGCCAGATGATTTCTCTGTTAACTCGGATG 2842  
Qy 2820 AATCATCGTCTCAGTATGTCAGCAAGGGTATCCTACACCAACAGATGATGCTCCCG 2879
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Db 2543 GT-----ATCAATCGATGCGAGCAAAA 2567
QY 2880 ATATGTATGATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGTCTGTCATC 2939
Db 2568 GTATGTGAATAGCGGTTTAGAAGTAGAAAAACCGTTCTGGTGAAGCG-----CATG 2617
QY 2940 CATTTGATTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATG 2999
Db 2618 AGTTCTCTATTCTATTGTATACAGGTGAAATCGATTACAAATGAAATGCAAGGAATATGGG 2677
QY 3000 TCTTATTAATAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTAGAGTCAATG 3059
Db 2678 TTGGATTAGATTACGGACCCAGAGGGATATGCAACATCGGAACCTTAGAATTTGGTCG 2737
QY 3060 AAGAAGGACCTAAACAGGTGAAGCATTTGGCAGATGTGAACAAAAAGGAAAGAAATGGA 3119
Db 2738 AAGAGGGACCTTTATCAGGAGACGCATTAGAACGCTTGCAAGAGAGAACAACACGTGGA 2797
QY 3120 AACACACATGGNAGAAAAACGTTGGGAAACACAAAGCCTTATGATCCAGCAAAACAGG 3179
Db 2798 AGATTCAATGTACAAGAAACGTTGAAGAAACAGATAGAGGTATATGGCATCGAAACAAG 2857
QY 3180 CTGTAGATGATTATTTACAAATGAACAAGAGTTACACTATCATATTTACTTTAGA----- 3234
Db 2858 CGGTAGATCGTTTATATGCGGATTATCAGGATCAGCACTGAATCTGTATGTAGAGATTA 2917
QY 3235 -TCATATTCAAAACGCTGATCGATCGGTACAGTFCGATTCCTTATGTATATACCAATTTGGT 3293
Db 2918 CAGATCTTACTGGGGCCCAAGATCTGATACAGTCCATTCTCTACGTATATATAACGAATGT 2977
QY 3294 TACCGAATGCTCAGGTATGAACATATGATGTATATCAAGATTAAACGACGCTATCATGC 3353
Db 2978 TCCAGAAATACACAGGGATGAACCTATACGAAGTTTACAGAAATTAACAGATCGCACTCCAAC 3037
QY 3354 AAGTTTATATTTATATGATGCACGAATGTCTATAACAAATGTGTGACTTTTACACAAGGAT 3413
Db 3038 AAGCGTGGAGTTTGTATGATCAGCGAATGCCAATGCCAATGGTGTATTTTCGNAATGGGT 3097
QY 3414 TACAGGGATGGCAGCAACAGGAAATGCCCGCGTACAAACAAATGGATGGAGCTTCAGTAT 3473
Db 3098 TAAGTAATTTGGAATGCAACGCTGGCGGTAGAAAGTTCGCAACAGATCAATCATCATCTGTCC 3157
QY 3474 TAGTTCTATCAATTCGAGCGCGGGGTATCTCAAAATTCGATCTCAAGATCATCATG 3533
Db 3158 TTGTGATTCCAAATCTGGGATGAGCAAGTTTCGCAACAGATTTACAGTTCAACCGAATCAA 3217
QY 3534 GATATGTGTATACGTGTGATTGCCAAAAAGAGGACCTGGAAAAAGGTATGTAAACGATGA 3593
Db 3218 GATATGTGTACAGTTACTGCGAGAAAGAGAGGGGTAGGAATGGATATGTAAATATCC 3277
QY 3594 TGGATTGTAATGAAAGCAGGAAACACTTAAGTTCACTTCTTTCGGAAGAG 3644
Db 3278 GTGATGGTGGAAATCAACAGAAACGTTACTTTTAGTGCAGCGATTATG 3328
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## RESULT 6

US-11-108-389-1

; Sequence 1, Application US/11108389

; Publication No. US20050261188A1

; GENERAL INFORMATION:

; APPLICANT: Andre R. Abad

; APPLICANT: Ronald D. Flannagan

; APPLICANT: Rafael Herrmann

; APPLICANT: Theodore W. Kahn

; APPLICANT: Albert L. Lu

; APPLICANT: Billy Fred McCutchen

; APPLICANT: James K. Presnail

; APPLICANT: James F.H. Wong

; APPLICANT: Cao-Guo Yu

; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal

; TITLE OF INVENTION: Activity

; FILE REFERENCE: 35718/291049

; CURRENT APPLICATION NUMBER: US/11/108,389

```
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3621
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3621)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Cry12Ib-1
US-11-108-389-1
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Query Match 5.1%; Score 307; DB 7; Length 3621;

Best Local Similarity 55.7%; Pred No. 1e-55;

Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;

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QY 2292 AATAAGCGAAAAAGGTTGTAGTCTTATGTTTCAAGTAGTAGTACGAAAAATACGTTAAAAA 2351
Db 2018 AAGCAGCGAAGAAAGACAGTGAATGCTTGTTTTAC--GAATACAAAAGATGGCTTACGAC 2074
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCATAGATGTATGTCCAGATG 2411
Db 2075 CAGGCGTAACCGATTATGAAGTGAATCAAGCGGCCAACTTACTGGAATGCCCTATCGGATG 2134
QY 2412 AACAAAAATCCTCAGGAAAAATAAATGTTATGGGATGAAATAAACTGGCAAAACAACTTA 2471
Db 2135 ATTTGTATCCAATGAAAAACGTTTGTATTGTATGTCAGTGAGAGGCGCAAAACGCTCA 2194
QY 2472 GTCACTCTCGTAAATCTACTCCAAATGGAGACTT-----TTCTGGGAATGATT 2519
Db 2195 GTGAGCAGCTAATTTGCTTCAAGATCCAGATTTCCAGAGATAAAATGGAGAAAAATGGCT 2254
QY 2520 GCACATTCCGTTAATGATATTATCATAGGATCCAATAAATCTATTTTAAAGGAAAAATTC 2579
Db 2255 GACGCGCAAGTACGGGAATTGAGGTTATAGAAAGGGATGCTTTATTCAAAGGCGGTTATC 2314
QY 2580 TACAGATCGTGGAGCAGAGACATATATGGAACCTCTATTTCCAACTTATCTGTCAAA 2639
Db 2315 TACGCTTACAGGTGGAGAGAAATAGATACGGMAACGTATCCAGGTATCTGTATCAA 2374
QY 2640 AAATAGATGAGTCTAAATTTAAAAACCATATACAGTTTTCGAGTAAAGAGGGTTTGGGAA 2699
Db 2375 AAGTAGAGGAGGTGTATTAAAAACCATACACAAGATATAGATTGAGAGGGTTTGTCCGAA 2434
QY 2700 GTAGTAAAGATTGAAATTAATGGTAAACAGTTACGGGAAAGAAATGTATGCTATCATGA 2759
Db 2435 GCAGTCAAGGATGGAAATTTTCACAATTCGTCA-----TCAACGAACCGAA 2482
QY 2760 ATGTTTCCAAATGATTTGGCCTATATGCAGCCTAACTCTTCATGTGGAGATTATCGCTGTG 2819
Db 2483 TTGTAAAAAATGTACCGGATGATTGTCTGCCAGATGTATCTCTCTGTAACTCGGATGTA 2542
QY 2820 AATCATCGTCTCAGTATGTGAGCCCAAGGATCTCTACCAACAGATGATGTCTCCCG 2879
Db 2543 GT-----ATCAATCGATGCGAGCAAAA 2567
QY 2880 ATATGTATGCATGCCCGCAAAATATAGTAGAAGCATGTGAAGTGTCAAGTCTGCATC 2939
Db 2568 GTATGTGAATAGCCGTTTAGAAGTAGAAAAACCGTTCTGGTGAAGCG-----CATG 2617
QY 2940 CATTTGATTTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATG 2999
Db 2618 AGTTCTCTATTCTTATTGATACAGGTGAATCGATTACAAATGAAATGCAAGGAATATGGG 2677
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Db 2930 CAGATCTTACTGGGCCCCAAGATCTGATACAGTCCATTCTCTACGTATATAACGAAATGT 2989  
Qy 3294 TACCGATGCTCCAGGTATCAACTATGATGTATATCAAGAGTTAAAGCGCAGGTATCATGC 3353  
Db 2990 TCCAGAAATACACAGGATCAACTATACGAAGTTTACAGAAATTAACAGATCGACTCCAAC 3049  
Qy 3354 AAGGTTATATATATGATGACGAAATGTCAACAAATGTGACTTTTACACAAAGGAT 3413  
Db 3050 AAGCGTGGAGTTGTATGATCAGGAAATGCCATACCAATGGTATTTTCGAATGGGT 3109  
Qy 3414 TACAGGATGGCAGCAGCAAGSAAATGCCCGGTACAAACAAATGGATGGAGCTTCAGTAT 3473  
Db 3110 TAAGTAATTGAATGCAACGCTGGCGTGAAGTACAAACAAATCAATCATACATCTGTCC 3169  
Qy 3474 TAGTCTCATCAATTTGGAGCGGGGGTATCTCAAACTTCGATGTCAAGATCATCATG 3533  
Db 3170 TTGTGATTCCAAATGGGATGAGCAAGTTTCGCAACAGATTTACAGTTCAACCGAATCAA 3229  
Qy 3534 GATATGTTTACGTGATTCGCAAAAGAAAGGACCTGGAAAGGTATGTAAACGATGA 3593  
Db 3230 GATATGTTTACGATTTACTGCGAAGAAAGAGGGGTAGGAATGGATATGTAAGTATCC 3289  
Qy 3594 TGGATGTAATGAAGACAGCAACACTTAAAGTTCACTTCTTCGGAAGAG 3644  
Db 3290 GTGATGTTGGAATCAACAGAAACGCTTACTTTTGTAGTCAAGCGATTATG 3340

## RESULT 9

US-11-058-727-17  
; Sequence 17, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 4874  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: Genomic DNA 1218-1  
US-11-058-727-17

Query Match 5.1%; Score 307; DB 7; Length 4874;  
Best Local Similarity 55.7%; Pred. No. 1.1e-55;  
Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;  
Qy 2292 ATAACGGAAAAAGGTTGTGAGTCCCTATGTTTCAAGTGTAGTACGAAAAATACGTTAAAAA 2351  
Db 2748 AAGCAGCGAAGAAAGCAGTGAATGCCTTGTGTAC---GAATACAAAAGATGGCTTACGAC 2804

Qy 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCCAATTTCTTATAGAAATGTATGTCAGATG 2411  
Db 2805 CAGCGCTAACGANTTATGAAGTGAATCAAGCGGCAAACTTAGTGGAAATGCCTATCGATG 2864  
Qy 2412 AACAAATCCTCAGGAAAAAATAATGTTATGGATGAAATAAAACTGGCAAAACAACTTA 2471  
Db 2865 ATTTGTATCCAAATGAAAAACGATTGTTATTTGATCGAGTGAGAGAGGCAAAACGCTCA 2924  
Qy 2472 GTCAAGTCTGTAATCTACTCCAAATGGAGACTT-----TTCTGGGAATGATTT 2519  
Db 2925 GTGAGGACAGTAATTTGCTTCAAGATCCAGATTTCCAGAGATAAATGGAGAAAAATGGCT 2984  
Qy 2520 GGACATTCGGTAATGATATATCATAGGATCCAAATCTCTATTTTAAAGGAAAAATTTTC 2579  
Db 2985 GAGCGCAAGTAGCGGAATTTAGGTTATAGAGGGGATGCTTTTATTCAAAGGCGGTATC 3044  
Qy 2580 TACAGATGCGTGGAGCA CGAGACATATATGGAACCTCTATTTTCCAACTTATATCTGTCAAA 2639  
Db 3045 TACGCTACAGGTGCGAGAGAAATAGATACGGAACGATATCCACGTATCTGTATCAAA 3104  
Qy 2640 AAATAGATGAGTCTAAATTTAAACCAATATACAGTTTATCGAGTAAGAGGTTTGTGGAA 2699  
Db 3105 AAGTAGAGGAAGGTGATTTTAAACCAATACACAGATATAGATTTGAGAGGGTTTGTGCGAA 3164  
Qy 2700 TAGTAGAAGATTTGAAATTTAAATGTTTACGCGGAAAGAAATTTGATGCTATCATGA 2759  
Db 3165 GCAGTCAGGATTTGGAATTTTCACAATTCGTCA-----TCAACGAAACGAA 3212  
Qy 2760 ATGTTCCAAATGATTTGGCTATATGACGCTTAATCCTTTCATGTGGAGATTAATCGCTGTG 2819  
Db 3213 TTGTAAAAAATGACCGGATGATTTGCTGCCAGATGTAATCTCTCTGTTAACTCGGATGGTA 3272  
Qy 2820 AATCATGCTCAGTATGTGAGCCAAAGGTATCTTACACCAACAGATGATATGCTCCCG 2879  
Db 3273 GT-----ATCAATCGATGCGAGCAACAAA 3297  
Qy 2880 ATATGTATGATGATCCCGCAAAATATAGATAGAAAGCATGTGAAGTCTCAGATCGTCAATC 2939  
Db 3298 GTATGTGATAGCCGTTTGAAGTAGAAGAACCGTTCTGTTGAAGCG-----CATG 3347  
Qy 2940 CATTTGATTTTCATATTTGACACCGGAGAGTAGATACAAATACAAATGATGATTTGATG 2999  
Db 3348 AGTTCTCTATTTCTTATGATACAGGTGAAATCGATTACAAATGAAATGCGGAAATATGG 3407  
Qy 3000 TCTTATTAATAATTTCTAATCCAGATGAGTACGCTACAGTAGGGAATCTAGAGTCAATG 3059  
Db 3408 TTGGATTTAAGATTACGGACCCAGAGGGATATGCAACACTCGGAAACCTAGAAATTTGGTCG 3467  
Qy 3060 AAGAAAGGACCACTAACAGGTGAAGCATTTGGCAGATGTGAAAACAAAAGGAAAGAAATGGA 3119  
Db 3468 AAGAGGACCTTTATCAGGAGACGATTTAGAACGCTTGGCAAGAGAGAGAACACAGTGGGA 3527  
Qy 3120 AACAAACATGAGAAAAAACCGTTGGGAAACACAAACGCTTATGATCCAGCAAAACAGG 3179  
Db 3528 AGATTCAAATGACAAAGACGCTGAAGAAACAGATAGAGGTATATGGCATCGAAACAAAG 3587  
Qy 3180 CTGTAGATGCATTTATTAACAAATGAACAGGTACACTATCATATTACTTTTGA----- 3234  
Db 3588 CGGTAGATCGTTTATATGCGGATTTATCAGGATCAGCAACTGAATCTCTGATGATGAGATTA 3647  
Qy 3235 -TCATATTCAAAAACGCTGATCGACTGGTACAGTCCCTTCCCTATGATATACCAATTTGGT 3293  
Db 3648 CAGATCTTACTCGGCGCCAGATCTGATACAGTCCCTTCTTACGTTATATACGAATGT 3707  
Qy 3294 TACCGAATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTTAAACGCAACGCTATCATGC 3353  
Db 3708 TCCAGAAATACACGGATGAACTATACGAAGTTTACAGAAATTAACAGATCGACTCCAAC 3767  
Qy 3354 AAGGTTATATTTATGATGACGAAATGTCAACAAATGCTGATCTTTTACACAAAGGAT 3413  
Db 3768 AAGCGTGGAGTTTGTATGATCAGCGAAATGCCATACCAATGCTGATTTTTCGAAATGGGT 3827  
Qy 3414 TACAGGTTGCGACCAACAGGAAATGCCGCGGTACCAACAAATGGAATGGATGAGCTTTCAGTAT 3473





Db 4008 GTGATGGTGGAAATCAACACAGAAACGCTTACTTTAGTGCAGACGATTATG 4058

## RESULT 11

```

RESULT 11
US-11-058-727-18
; Sequence 18, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6613
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Genomic Cry12I8-2
US-11-058-727-18

Query Match          5.1%; Score 307; DB 7; Length 6613;
Best Local Similarity 55.7%; Pred. No. 1.3e-55;
Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;

QY      2292  AATAAGCGAAAAAGTTGTGCAGTCCTATGTTTACAGTAGTACGAAAAATACGTTAAAAA 2351
DB      3283  AAGCAGCGAAGAAGCAGTGAATGCCCTGTGTTAC---GAATACAAAAGATGGCTTACGAC 3339

QY      2352  TAGAAGCAGCAGATTTATGAATAGATCAACGGCGCATTTCTATAGAAATGATGTGCAGATG 2411
DB      3340  CAGGCGGTAAACGGATTATGAAGTGAATCAAGCGGCAAACTTAGTGGGAATGCTATCGGATG 3399

QY      2412  AACAAAATCCTCAGGAAAAAATATGTTATGGATGAAATAAACTGGCAAAACAACTTA 2471
DB      3400  ATTTGTATCCAATGA AAAACGATGTGTTATTTGATGTCAGTGAGAGAGCAAAACGGCTCA 3459

QY      2472  GTCAGTCTCGTAATCTACTCAAAATGGAGACTT-----TTCTGGGAATGATT 2519
DB      3460  GTGAGGCACGTAATTTGCTTCAAGATCCAGATTTTCCAAGAGATAAATGGAGAAAAATGGCT 3519

QY      2520  GGCATTCGGTAATGATATTTATCATAGGATCCAATAATCTATTTTAAAGGAAAAATTC 2579
DB      3520  GGACGGCAAGTACCGGGAATTTAGGTTTATGAAGGGGATGCTTTTATTCAAAGGCGGTTATC 3579

QY      2580  TACAGATGCGGTGGAGCAGCAGACATATATGGAATCTTATTTCCAACCTATATCTGTCAAA 2639
DB      3580  TACGCCTCAGGTGGAGAGAAATAGATACGGAACGATATCCAAAGTATCTGTATCAA 3639

QY      2640  AAATAGATAGTCTAAATTTAAACCATATACAGTTATCGAGTAAAGGGTTTTGTGGAA 2699
DB      3640  AAGTAGAGGAAGGTGTTATTTAAACCATATACAGATATAGATTGAGAGGGTTTTGTGGAA 3699

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|    |      |  |      |
|----|------|--|------|
| Qy | 2700 | GTAGTAAAGATTGAAATTAAATGGTAAACAGTTTACGGGAAAGAAATTTGATGCTATCATGA     | 2759 |
| Db | 3700 | GCAGTCAAGGATTGGAAATTTTTCACAAATTCGTCA-----TCAAACGAACCGAA            | 3747 |
| Qy | 2760 | ATGTTCCAAATGATTTGGCCCTATATCAGCGCTAATCCTTTCATGTGGAGATTATCGCTGTG     | 2819 |
| Db | 3748 | TTGTAAAAAATGTACCGGATGATTTGCTGCCAGATGTATCTCTGTTAACTCCGATGGTA        | 3807 |
| Qy | 2820 | AATCATCGTCTCAGTATGTGAGCCAAAGGGTATCCTACACCAACAGATGGATATGCTCCCG      | 2879 |
| Db | 3808 | GT-----ATCAATCGATGCAGCGAACAAAA                                     | 3832 |
| Qy | 2880 | ATATGTATGATGCCCGCAAAATATAGATAGAAGCATGTGAAGTGTCAAGTCGTCAATC         | 2939 |
| Db | 3833 | GTATGTGAATAGCGGTTTAGAAGTAGAAAAACCGTCTCTGGTGAACG-----CATG           | 3882 |
| Qy | 2940 | CATTGTGATTTTCATATTGACACCGGAGAGTAGATACAAATACAAATGTAGGTATTGATG       | 2999 |
| Db | 3883 | AGTTCTCTATTCTTATTTGATACAGGTGAATTCGATTACAAATGAANAATGCAAGGAATATGGG   | 3942 |
| Qy | 3000 | TCTTATTTAAAAATTTCTTAATCCAGATGGATACGCTACAGTAGGGAAATCTAGAAAGTCATTG   | 3059 |
| Db | 3943 | TTGGATTTAAGATTACGGACCCAGAGGGATATGCAACACTCGGAACCTTAGAATTTGGTCG      | 4002 |
| Qy | 3060 | AAGAAGGACCACTAAACAGGTGAAGCATTTGGCCATGTGAAACAAAAGGAAAGAAATGGGA      | 3119 |
| Db | 4003 | AAGAGGACCTTTTATCAGGAGACGCATTAGAACCGTTGCAAGAGAGAACAACACAGTGGGA      | 4062 |
| Qy | 3120 | AACAAACATGGAGNAANAACGTTGGGNAACACAAACAGCCTATGATCCAGCAAAACAGG        | 3179 |
| Db | 4063 | AGATTCAATTGACAAGAAAGCGTGAAGAAACAGATAGAAGGTATATGGCATCCGAACCAAG      | 4122 |
| Qy | 3180 | CTGTAGATGCATTTATTTTACAAATGAAACAAGAGTTTACACTATCATATTTACTTTTAGA----- | 3234 |
| Db | 4123 | CGGTAGATCGTTTATATGCCGATTATCAGGATCAGCAACTGTAATCTCGATGTAGAGATTA      | 4182 |
| Qy | 3235 | -TCATATTCAAAACGCTGATCGACTGGTACAGTCGATTCCTCTATGTATACCATTAATTGGT     | 3293 |
| Db | 4183 | CAGATCTTACTCGGGCCCAAGATCTGATACAGTCCATTCCTTACGTATATAACGAAATGT       | 4242 |
| Qy | 3294 | TACCGAATGCTCCAGGTATGAACTATGATGTATATCAAGAGTTTAAACGCAAGTATCATGC      | 3353 |
| Db | 4243 | TCCAGAAATACACGGATGACTATACGAAAGTTTACAGAAATTAACAGATCGACTCCAC         | 4302 |
| Qy | 3354 | AAGGTTATTAATTTATATGATGCAAGAAATGCTATAACAAATGCTGACTTTTACACAAGGAT     | 3413 |
| Db | 4303 | AAGCGTGGAGTTTGTATGATCAGCGAAATGCCATACCAATGCTGATTTTCGAAATGGGT        | 4362 |
| Qy | 3414 | TACAGGATGGCAGCGACAGGAAATCCCGCGGTACAAACAAATGGATGGAGCTTCAGTAT        | 3473 |
| Db | 4363 | TAAAGTAATTTGSAATGCAACCGCTCGGGGTAGAAGTACAAACAAATCAATCATACATCTGTCC   | 4422 |
| Qy | 3474 | TAGTTCTATCAAAATTCGAGCGCGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATG       | 3533 |
| Db | 4423 | TTGTGATTCCAAATCGGATGACAAAGTTTCGCACAGTTTACAGTTTCAACCGAATCAAA        | 4482 |
| Qy | 3534 | GATATGTGTTTACGTGTGATTTGCCAAAAAAGAGGACCTCGAAAGAGGTATGTAAACGATGA     | 3593 |
| Db | 4483 | GATATGTGTTTACGATTTACTGCCAGAAAGAGGCGGTAGGAATGGATATGTAAAGTATCC       | 4542 |
| Qy | 3594 | TGGAATTTGAATGGAAGACGAGGAAACATTAAATTTCATCTTCTCGGAAGAG               | 3644 |
| Db | 4543 | GTGATGGTGGAAATCAAAACAGAAACGCTTACTTTTATGTCGAACGCAATTATG             | 4593 |

RESULT 12.  
US-11-108-389-18  
; Sequence 18, Application US/11108389  
; Publication No. US2005026118A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann

```
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6613
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic Cry12Ib-2
US-11-108-389-18

Query Match          5.1%; Score 307; DB 7; Length 6613;
Best Local Similarity 55.7%; Pred. No. 1.3e-55;
Matches 763; Conservative 0; Mismatches 530; Indels 78; Gaps 6;

QY 2292 AATAAGCGAAAAAGGTGTGAGTCCCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA 2351
DB 3283 AAGCAGCGAAGAAAGCAGTGAATGCCCTGTGTAC---GAATACAAAAGATGCTTACGAC 3339
QY 2352 TGAAACGACAGATTATGAATAGATCAAGCGGCCAATTTCTATAGAAATGATGTAGATG 2411
DB 3340 CAGGCGTAACGGATTATGAATGAATCAAGCGGCAAACTTAGTGAATGCCATCGGATG 3399
QY 2412 AACAAATCCTCAGGAAAAAATAGTTATGGATGAAATAACTGGAACAACTGCAAAACACTTA 2471
DB 3400 ATTGTATCAATGAATGAATCAAGATTGTTATTTGATCGAGTAGAGGCAAAACGCTCA 3459
QY 2472 GTGAGTCTGTAATCTACTCCAAAATGGAGACTT-----TTCTGGGAATGATT 2519
DB 3460 GTGAGGCACGTAATTTGCTTCAAGATCCAGATTCCAGAGATAAATGGAGAAATGGCT 3519
QY 2520 GGACATTCGGTAAATGATATATATATAGGATCCAAATATCTATTTTAAAGGAAAAATTC 2579
DB 3520 GGACGGCAAGTACGGGAATTTAGGTTATAGAGGGGATGCTTTATTTCAAAGGGCGTTATC 3579
QY 2580 TACAGATCGTGGACGACGACATATATATGGAATCTTATTTCCAACTATATCTGTCAA 2639
DB 3580 TAGCCCTACAGGTGCGAGAGAAATAGATACGGAACGATATCCAACTATCTGTATCAA 3639
QY 2640 AATAGATGAGTCTAAATTAATAAACCATATACAGTTTATCGAGTAAGAGGTTTGTGGGAA 2699
DB 3640 AAGTAGAGGAGGTGATTAAACCATATACAGATATAGATTGAGAGGTTTGTTCGAA 3699
QY 2700 GTAGTAAAGATTGAAATTAATGGTAACAGTTTACGGGAAAGAAATATGATGCTATCATGA 2759
DB 3700 GCAGTCAAGGATTGGAATTTTCACAATTCGTCA-----TCAACGAAACCGAA 3747
QY 2760 ATGTTCCAAATGATTTGGCCTATATCATGAGCTAATCTTTCATGTGAGATATCGCTG 2819
DB 3748 TTGTAATAAATGATPACCGGATGATTGCTGCCAGATGATCTCTGTTAACTCGATGGTA 3807
QY 2820 AATCATCGTCTCAGTATGTGAGCAAGGGGTATCCTACACCAACAGATGGATATGCTCCCG 2879
DB 3808 GT-----ATCAATCGATGCGAGCAACAAA 3832

; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6613
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Genomic Cry12Ib-2
US-11-108-389-18

QY 2880 ATATGTATGCATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCAAGTCTCATC 2939
DB 3833 GTATGTGAATAGCCGTTTATAGAAAGTGAAGAACCGTTCTGTTGAAGCG-----CATG 3882
QY 2940 CATTTTGAATTTTCAATTCACACCGGAGAGTAGATACAAATACAAATGTAGTATTTGATG 2999
DB 3883 AGTTCTCTATTTCTTATTTGATACAGGTGAATTCGATTACAAATGAATTCGAGGAATATGG 3942
QY 3000 TCTTATTTAAAAATTTCTAATCCAGATGGATAGCTTACAGTAGTGGGAAATCTAGAGTCA 3059
DB 3943 TTGGATTTTAAGATTACGGACCCAGAGGGGATATGCAACACTCGGAAACCTAGAAATTTGG 4002
QY 3060 AAGAAGGACCACTAAACAGGTGAAGCATTTGGCACATGTGAAACAAAGAAAGAAATGGA 3119
DB 4003 AAGAGGGACCTTTATCAGGAGACGCATTTAGAACCGTTTGCAAAGAGAAACCAACAGTGG 4062
QY 3120 AACACACATATGAGAAAAAAGCTTGGGAAAAACAAACAGCCCTATGATCCAGCAAAACAGG 3179
DB 4063 AGATTCAATGACAAAGAACAGCTGAGAAACAGATAGAGGTATATGGCATCGAAACAG 4122
QY 3180 CTGTAGATGCATTATTTTAAATGAACAGAGTTTACATCATCATATTTAGTACTTTAG 3234
DB 4123 CGGTAGATCGTTTATATATCGGATTATCAGGATCAGCAACTGAATCCTGATGTAGAGATTA 4182
QY 3235 -TCATATTTCAAAAACGCTGATCGACTGGTACAGTGGATTTCCCTATGTATACCATATTTGGT 3293
DB 4183 CAGATCTTTACTGCGGCCCAAGATCTGATACAGTCCATTTCTTTACGTATATTAACGAAATGT 4242
QY 3294 TACCGAATGCTCCAGGTATGAATGATGATATCAAGAGTTTAAACGACGATCATGTC 3353
DB 4243 TCCGAGAATACCAGGAGTGAATATATACGAAGTTTACAGAAATTAACAGATCGACTTCAAC 4302
QY 3354 AAGGTTATATTTTATATGATGACGAAATGTCAAAACAAATGGTGGTACTTTTACACAAAGAT 3413
DB 4303 AAGCGTGGAGTTTGTATGATCAGCGAAATGCCATACCAAAATGGTGGTATTTTGAATGGT 4362
QY 3414 TACAGGATGGACGCAACAGAAATCGCGGGTACACAAATGATGATGAGGCTTCAGTAT 3473
DB 4363 TAAGTAATTTGGAATGCAACGCTGCGTAGAAGTACAAACAAATCAATCATATCTGTCC 4422
QY 3474 TAGTTCTATCAATTTGGAGCGCGGGGTATCTCAAAAACCTTGATGCTCAAGATCATGTC 3533
DB 4423 TTGTGATTTCCAAACTGGGATGAGCAAGTTTCCCAACAGTTTACAGTTCAACCGAATCAA 4482
QY 3534 GATATGTTTACGTGTGATTTGCCAAAAAGAGGACCTCGGAAAAAGGGTATGTAACGATGA 3593
DB 4483 GATATGTTTACGAGTTACTGCGAGAAAGAGGGGTAGGAAATGGATATGTAAGTATCC 4542
QY 3594 TGGATTGTAATGGAAGCAGGAAACACATTAAGTTTCACTTCTTTCGCAAGAG 3644
DB 4543 GTGATGGTGGAAATCAAAACAGAAACGCTTACTTTTAGTGAACGCGATTATG 4593

RESULT 13
US-11-070-575-4
; Sequence 4, Application US/11070575
; Publication No. US20050271642A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shin-ichiro
; APPLICANT: NOZAWA, Mikiko
; APPLICANT: BANDO, Hisanori
; TITLE OF INVENTION: RECOMBINANT ORGANISMS PRODUCING INSECT
; TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
; FILE REFERENCE: 59562200300
; CURRENT APPLICATION NUMBER: US/11/070,575
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: US 60/549,094
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4119
; TYPE: DNA
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| ; ORGANISM: Bacillus popilliae                                   |   | us-10-781-979-1.1.rnpbn   |      |
| US-11-070-575-4  |   |   |      |
| Query Match 5.0%; Score 301; DB 7; Length 4119;                  |   |   |      |
| Best Local Similarity 55.4%; Pred. No. 2e-54;                    |   |   |      |
| Matches 819; Conservative 0; Mismatches 530; Indels 130; Gaps 7; |   |   |      |
| Qy   | 2292 AATAAGCGAAAGGTTGTGAGTCTCTATGTTTACAGTAGTACGAAATAACGTTAAAAA      | 3000 AGCAGCAGCTGTTTCGCAACGAAACACAAATATGATCGCGCAACACATGCGGTGATGGGT     | 3059 |
| Db   | 2043 AAAAAGCAAGGAACGGTGAACCAATTTGTTTACAGATGATCGAAAGAGGCGCTAAAG      | 3192 TATTTTACAAA-----TGAACAAGAGTTACACTATCATATTTACTTTTAGATCATATTTCAA   | 3245 |
| Qy   | 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATAGAAATGATGTCAGATG    | 3060 TATTTTACAAACACGCGCTATGAAAAATTTGAAGTTTCAAAACAAACCATCTCCAATATTTTGT | 3119 |
| Db   | 2103 AAGACACGACCGATTATGAGATTGATCAAGCGCGCAACGGTGGTAGATTGTATATCGGATG  | 3246 ACCTGATGACATGGTACAGTCCCTATGTTTATGATACCAATAATTTGGTTTACCGAATGCTC   | 3305 |
| Qy   | 2412 AACAAAATCTCAGGAAATAATATGTTATGGGATGAAATAAAACTGGCAAAACAATTTA     | 3120 ATGCTGATCATCTCGTGCAGTCCGATTTCTTATGTTATATAATAATATGTACCGGAAGTTC    | 3179 |
| Db   | 2163 ---AGTGTGACATGAGAAAATGATCTCTGTAGATGAAGTAAAAATATGCAAAAACAATCA   | 3306 CAGGTATGAACATATGATATATCAAGAGTTAAACGACGCTATCATGCAAGGTTTATAATT     | 3365 |
| Qy   | 2472 GTCAGTCTCTGTAATCTACTCCAAAATGGAGACTTTTCT-----                   | 3180 CAGGTATGAATTTACGAACCTCTATTCAGAGCTAAACACACTGGTTTCAGAAATGCGTTCTACC | 3239 |
| Db   | 2220 GCCAAGCCCGCAATTTACTGCTCAATGGGAATTCGATGATCTATATCCAGTCTGGAGA     | 3366 TATATGATGACAGAAATGTCATAACAAAATGCTGACATTTACACAGGATTTACAGGGATGGC   | 3425 |
| Qy   | 2510 ---GGGAATGATGACATTCGGTAAATGATATATCATAGGATCCAAATCTTATTTTAA      | 3240 TGTATGACCCAGCGGAATCTGATTTAAAAAGGGCG-CTTTAGCAATGGGCTTATGTATTGGC   | 3298 |
| Db   | 2280 GGGAGAATCCATGCAAAAACAAGTCCGAATGTTTACGATCCGTCGAGATAACCCGATTTTAA | 3426 ACCCAACAGGAAATGCGCGGTACAAACAATGATGGAGCTTCAGTATTAGTTCTATCAA       | 3485 |
| Qy   | 2568 AAGGAAATTTCTACAGATCGGTGGAGCAAGAGACATATATGGAC-----TCTATTTC      | 3299 AAGCTGCCCTCATGCAAGTAGAGCAAGAAATTTGAGAAATCGGTCTCGTCTGCGCAA        | 3358 |
| Db   | 2340 AAGGCCATTATCTCAGTATCGCGGGTCGAAACGATATCGAGGCCACAATGATACCTTCC    | 3486 ATTTGAGCGCGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATGGAATATGTGTATC     | 3545 |
| Qy   | 2622 CAACCTATATCTGTCAAAAATAGATGAGTCTAAATTTAAACCATATACACGTTATCGAG    | 3359 ATTTGGGATGCCAATGTTGCGCAAGATCTTTGTTATCGAACACAAATCGCGTTATGTATTC    | 3418 |
| Db   | 2400 CCAGGTATGCTATCAAAAATAGACGAGCCAAATTTAAGCCGTATACAGTTTATAAG       | 3546 GTGTGATTCGCAAAAAGAGGACCTTGGAAAAGGGTATGTAACGATGATGGATTGTATG       | 3605 |
| Qy   | 2682 TAAGAGGGTTTGTGGGAAGTAGTAAAGATTGAAATTAATGGTAACACGTTACGGGAAAG    | 3419 GTGTCACGCGAGAAAAGAGATCCGGGAGCTGGCAATGTTTACCTTTAGTGACTGTGAAA      | 3478 |
| Db   | 2460 TGGCGGGTTTGTGGCAGCAGCAAGCTCTAGAGCTGTTGGTTTACAGCTATAATGAAG      | 3606 GAAAGCAGGAAACACATTAAGTTTACATCTTCTTTCGCGAAGAAG 3644               |      |
| Qy   | 2742 AATTTGATGCTATCATGAATGTTTCCAAATGATTTGGCTATATGCGCCTAATCCCTTCAT   | 3479 ATCATGTGCAACAAGCTGAGCTTTTACTTTCTTGGCATATAG 3517                  |      |
| Db   | 2520 AAGTCGATGCGATTTTAGATGTACCGGATAATATCCCGCATGCGCGCATACCTGTCTGCG   |   |      |
| Qy   | 2802 GTGAGATTTATCGTGTGAATCATCGTC-----TCAGTATGAGCCAA 2845            |   |      |
| Db   | 2580 GTGAATTTGATCGATGCAAGCCCTATTCGTATCCACCTTTACTTCCGAATGTAAACCTG    |   |      |
| Qy   | 2846 GGSTA-----   |   |      |
| Db   | 2640 AGTTTATAAATCAGATGCAACCATCTCTTTGCCACCACTCAGATGGTCTGATTACAATA    |   |      |
| Qy   | 2851 -----TCCTACCAACAGATGATATGCTCCGGATATGATGTCAT 2891               |   |      |
| Db   | 2700 ACATGAACATGACGACGAGTACTACCATGAATCCTACCTTTAGCCCTGAAATAGCATCCA   |   |      |
| Qy   | 2892 GCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTACGATCGTCAATTCATTTGATTTTC   |   |      |
| Db   | 2760 GCCAAGTGAATTCGGCAGAAAACATCGCAATGTATCATAGCGCATCAATTTGAGTTCC     |   |      |
| Qy   | 2952 ATATTGACCGGAGAGTAGATACAAATACAAAATGATGAGTATTTGATGTTTATTAATAA    |   |      |
| Db   | 2820 ATATTGATCGGCAACATCGATCTGTCGAAGATTTGGGCCCTATGGGTGATCTTCAAAA     |   |      |
| Qy   | 3012 TTTCTAATCAGATGATGATGCTACAGTAGGGAATCTAGAAATGATGAAAGAGGACCAAC    |   |      |
| Db   | 2880 TCTGTGCCACAGATGGTTACGCAAGCTTAGATGTTTGGAAATGATTTGAAGAGGAGCGC    |   |      |
| Qy   | 3072 TAACAGGTGAAGCATTTGGCAGATGTGAAACAAAGGAAGAAATGGAACACACATGG 3131  |   |      |
| Db   | 2940 TGGGTGTCGAAGCATTTAGAACTTGTCAAGAAAAGAAAAGAAATGGAGCATCAGAAGG     |   |      |
| Qy   | 3132 AGAAAAACGTTGGGAAACACAAACAGCCTTATGATCCAGCAAAACAGGCTGTAGATGTCAT  |   |      |

RESULT 14  
US-11-091-643-1  
; Sequence 1, Application US/11091643  
; Publication No. US20050246789A1  
; GENERAL INFORMATION:  
; APPLICANT: TANAKA, Masao  
; APPLICANT: YOKOYAMA, Tomoko  
; APPLICANT: AOYAGI, Morichi  
; APPLICANT: HASEGAWA, Makoto  
; APPLICANT: EHARA, Gaku  
; APPLICANT: KIMURA, Masaharu  
; APPLICANT: NISHIHASHI, Hideji  
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
; TITLE OF INVENTION: polynucleotide encoding the same  
; FILE REFERENCE: OPI335  
; CURRENT APPLICATION NUMBER: US/11/091,643  
; PRIOR FILING DATE: 2005-03-29  
; PRIOR APPLICATION NUMBER: JP 2001-115754  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: JP 2001-203463  
; PRIOR FILING DATE: 2001-07-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Bacillus popilliae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(402)  
US-11-091-643-1  
  
Query Match 2.6%; Score 152.8; DB 9; Length 402;  
Best Local Similarity 63.2%; Pred. No. 2.1e-23;  
Matches 254; Conservative 0; Mismatches 142; Indels 6; Gaps 1;  
  
Qy 2909 AGAAGCATGTGAAGTGTCAAGTCTCATCTTTCATTTTTCATATTGACACCGGAGAA 2968

Db 1 AGAAAAACCGCAAAATGTATCAAGCGCATCAATTTGAGTTCATATTGATACCGGGACA 60  
QY 2969 GTAGATACAAATACAAATGTAGTATTTGATGTCTTATTAATAAATTTCTAATCCAGATGGA 3028  
Db 61 ATCGATCTGGTCGAAGATTTGGGCATTTGGGTGATCTTCANAATCTGTGCCACAGATGTT 120  
QY 3029 TAGCGTACAGTAGGGAATCTAGAAAGTCATTTGAAGAGGACCACTAAACAGGTGAAGCATTTG 3088  
Db 121 TAGCGCAAGCTTAGATGATTTGGAAGTGATTTGAAGAAGGAGCGCTGGGTGTGGAAGCATTTA 180  
QY 3089 GCACATGTGAAACAAAGGAAGAATGGAACACACATGAGAGAAAAAGCTTGGGAA 3148  
Db 181 GAACTTTGTCAAGAAAAAGAAAAAGAAATGGAGACATCAGAAGGAGAGCACTGTTCCGAA 240  
QY 3149 ACACAAACAGCCCTATGATCCAGCAAAACAGGCTGTAGATGCATTATTTACAAA-----T 3202  
Db 241 ACGAACAACAAATATGATGGGCGCAACACGCGGTGATGGCGTTATTCACAAACACGCGC 300  
QY 3203 GAACAAGAGTTACATCATATCATATTTACTTTAGATCATATTTCAAACCGCTGATCGATGTTA 3262  
Db 301 TATGAATAAATTTGAATTCGAAACCAACCATCTCCAATATTTTGTATGCTGATCATCTCGTG 360  
QY 3263 CAGTCGATTCCTCTATGATATACCATTAATTTGGTTACCGAATGCT 3304  
Db 361 CAGTCGATTCCTTATGATATATAATAATAATATGTACCGGAAGTT 402

RESULT 15

US-11-058-727-15  
; Sequence 15, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; CURRENT FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 1860  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (truncated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)...(1860)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: 49PVD  
US-11-058-727-15

Query Match 1.5%; Score 87.8; DB 7; Length 1860;  
Best Local Similarity 59.2%; Pred. No. 2.4e-09;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;  
QY 881 TGATTACTATGACGGATTAATAATGCAAAACGGCAGAGATATACCAATATTGTTTATATTC 940

Db 555 TAACTATTATGATCGTCAAACTTACTGCAAGATATTCTGATCACTGTGTAAAGTG 614  
QY 941 GTATCAGGTAGGTTTAAATTCAGATAAAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAA 1000  
Db 615 GTATGAAACTGGTTTTCGCAAAATTAATA-----GGCAGGAGCGCTAAACAATGGGTTCA 668  
QY 1001 ATTTAATAAATTTCTAGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCC 1060  
Db 669 CTATAACCAATTCCTAGAGAAATGACACTGGCGGTTTTAGATGTTTGTTCATTATTATCCC 728  
QY 1061 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTA 1120  
Db 729 AAAATTATGACACACACGACGATACCCCAATGAAACGAAAGCAACCTAAACAAGGAAGTATA 788  
QY 1121 TACAGATGAGTGGGATATTTATCGGGAACCTTATAGTTGGTTTACCGAAT 1169  
Db 789 TACAGATCCACTGGGCGGCTAAACGTCTCTTCAATTGGTTCCTGGTAT 837

Search completed: December 20, 2005, 04:58:15  
Job time : 410.161 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: December 19, 2005, 13:41:30 ; Search time 683.153 Seconds  
(without alignments)  
15559.937 Million cell updates/sec

Title: US-10-781-979-1  
Perfect score: 5980  
Sequence: 1 tacatgaataacataaagag.....ttctaaaagcctctgtat 5980

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1303057 seqs, 88878028 residues  
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq: \*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq: \*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfilee1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description       |
|------------|-------|---------------|--------|-------|-------------------|
| 1          | 765.8 | 12.8          | 3543   | 3     | US-09-224-024-27  |
| 2          | 765.8 | 12.8          | 3543   | 6     | PCT-US94-07902-27 |
| 3          | 380.8 | 6.4           | 3504   | 3     | US-10-089-678-2   |
| 4          | 380.8 | 6.4           | 3690   | 3     | US-10-089-678-3   |
| 5          | 358   | 6.0           | 3797   | 2     | US-07-915-203-1   |
| 6          | 358   | 6.0           | 3797   | 2     | US-08-272-887-1   |
| 7          | 358   | 6.0           | 3797   | 2     | US-08-789-449-1   |
| 8          | 314.6 | 5.3           | 3471   | 2     | US-07-876-280-29  |
| 9          | 314.6 | 5.3           | 3471   | 2     | US-07-812-180A-1  |
| 10         | 314.6 | 5.3           | 3471   | 2     | US-08-315-468-1   |
| 11         | 314.6 | 5.3           | 3471   | 3     | US-07-941-650A-1  |
| 12         | 308.2 | 5.2           | 3726   | 3     | US-09-001-982-11  |
| 13         | 308.2 | 5.2           | 3726   | 3     | US-09-668-650-11  |
| 14         | 305.4 | 5.1           | 3414   | 2     | US-07-973-320-3   |
| 15         | 302.2 | 5.1           | 3414   | 2     | US-07-973-320-1   |
| 16         | 288.4 | 4.8           | 3507   | 2     | US-08-315-468-3   |
| 17         | 278.4 | 4.7           | 3759   | 2     | US-08-542-921-1   |
| 18         | 278.4 | 4.7           | 3759   | 2     | US-08-880-685-1   |
| 19         | 278.4 | 4.7           | 3759   | 2     | US-08-880-684-1   |
| 20         | 276.4 | 4.6           | 3522   | 2     | US-08-040-751-4   |
| 21         | 276.4 | 4.6           | 3522   | 2     | US-08-291-368-1   |
| 22         | 276.4 | 4.6           | 3522   | 2     | US-08-962-190-1   |
| 23         | 276.4 | 4.6           | 3522   | 6     | PCT-US95-10310-1  |
| 24         | 276.4 | 4.6           | 3522   | 9     | 5164180-3         |

|    |       |     |      |   |                   |                   |
|----|-------|-----|------|---|-------------------|-------------------|
| 25 | 275.6 | 4.6 | 3468 | 3 | US-09-001-982-9   | Sequence 9, Appli |
| 26 | 275.6 | 4.6 | 3458 | 3 | US-09-668-650-9   | Sequence 9, Appli |
| 27 | 275.6 | 4.6 | 3471 | 3 | US-09-002-285-71  | Sequence 71, Appl |
| 28 | 275.6 | 4.6 | 3471 | 3 | US-09-589-477-71  | Sequence 71, Appl |
| 29 | 275.6 | 4.6 | 3471 | 3 | US-10-099-285A-71 | Sequence 39, Appl |
| 30 | 273.2 | 4.6 | 3504 | 3 | US-09-661-322A-39 | Sequence 4, Appli |
| 31 | 271.8 | 4.5 | 4344 | 2 | US-08-532-547-4   | Sequence 4, Appli |
| 32 | 271.8 | 4.5 | 4344 | 2 | US-08-379-656B-4  | Sequence 4, Appli |
| 33 | 271.8 | 4.5 | 4344 | 3 | US-08-455-838-4   | Sequence 4, Appli |
| 34 | 271.8 | 4.5 | 4344 | 3 | US-09-019-809-4   | Sequence 4, Appli |
| 35 | 271.8 | 4.5 | 4344 | 3 | US-09-471-177-4   | Sequence 4, Appli |
| 36 | 271.8 | 4.5 | 4344 | 3 | US-09-220-806-4   | Sequence 4, Appli |
| 37 | 270.8 | 4.5 | 3453 | 3 | US-09-002-285-75  | Sequence 75, Appl |
| 38 | 270.8 | 4.5 | 3453 | 3 | US-09-589-477-75  | Sequence 75, Appl |
| 39 | 270.8 | 4.5 | 3453 | 3 | US-10-099-285A-75 | Sequence 75, Appl |
| 40 | 270.2 | 4.5 | 3504 | 2 | US-08-291-368-3   | Sequence 3, Appli |
| 41 | 270.2 | 4.5 | 3504 | 2 | US-08-962-190-3   | Sequence 3, Appli |
| 42 | 270.2 | 4.5 | 3504 | 6 | PCT-US95-10310-3  | Sequence 73, Appl |
| 43 | 270   | 4.5 | 3471 | 3 | US-09-002-285-73  | Sequence 73, Appl |
| 44 | 270   | 4.5 | 3471 | 3 | US-09-589-477-73  | Sequence 27, Appl |
| 45 | 270   | 4.5 | 3471 | 3 | US-09-661-322A-27 |                   |

ALIGNMENTS

RESULT 1  
US-09-224-024-27  
; Sequence 27, Application US/09224024  
; Patent No. 6056953  
; GENERAL INFORMATION:  
; APPLICANT: Leslie Hickie  
; APPLICANT: Jewel Payne  
; TITLE OF INVENTION: Materials and Methods for the Control of  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/224,024  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/856,226  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA79  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3543 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-224-024-27  
Query Match 12.8%; Score 765.8; DB 3; Length 3543;  
Best Local Similarity 71.5%; Pred. No. 2.2e-161;

Matches 1058; Conservative 0; Mismatches 397; Indels 24; Gaps 3;  
QY 2292 AATAACGCAAAAGGTTGTGAGTCTCTATGTTTACAAGTAGTAGTACGAAAAATACGTTAAAAA 2351  
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QY TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGATGTCAGATG 2411  
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DB 2132 CAGAACTTACAGATTATGACATAGATCAAGCGCCAAATCTTTGTGGAATGATTTCTCTGAAG 2191  
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DB 2660 ATTCAATGCAATATGATACAGGGAAGAAAGCATGCTGTATGTTCAGGATTTCCATCAATTA 2719  
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DB 3080 ATGTTCCAGGTATGAATTTATGATATCTATGTAGATTTGGATGTCAGGTGGCAAGCGC 3139

QY 3360 ATAATTTATATGATGACGAGAAATGTCTAAACAAATGGTACTTTTACAAAGGATTCACAG 3419  
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DB 3140 GTTATTTGTATGATACAAAGAAATATTTAAAAATGGTGATTTTACAAAGGGTAAATGG 3199  
QY 3420 GATGCGACGCAACAGAAATGCGCGGTACAAACAAATGGATGGAGCTTCAGTATTAGTTTC 3479  
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DB 3200 GGTGCGATGTAACTGGAATGCGAGACGTACAAACAAATAGATGGTGTCTGTATTGGTTTC 3259  
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DB 3260 TATCTAATTTGGAGTGTGCGGTATCTCAAAATGTCACTCCAACTATCATGGGTATG 3319  
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DB |||||  
DB 3440 CAGTAGATGATTTCCAGATACAGATCGTGACGAAATGAGATAGCGGAACCGAAGGTT 3499  
QY 3720 CATTTTATATAGATAGCATCGAGTTGCTTTGTATGCAAG 3758  
DB |||||  
DB 3500 CGTTTTATATCGAAAGCATTTGAATTAATTTGTCATGAACG 3538

## RESULT 2

PCT-US94-07902-27

; Sequence 27, Application PC/TUS9407902

; GENERAL INFORMATION:

; APPLICANT: Street address: 4980 Carroll Canyon Road

; APPLICANT: City: San Diego

; APPLICANT: State/Province: California

; APPLICANT: Country: US

; APPLICANT: Postal code/Zip: 92121

; APPLICANT: Phone number: (619) 453-8030

; APPLICANT: Telex number: 92121

; TITLE OF INVENTION: Materials and Methods for the Control of

; TITLE OF INVENTION: Calliphoridae Pests

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David R. Saliwanchik

; STREET: 2421 N.W. 41st Street, Suite A-1

; CITY: Gainesville

; STATE: FL

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07902

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Saliwanchik, David R.

; REGISTRATION NUMBER: 31,794

; REFERENCE/DOCKET NUMBER: MA79

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 904-375-8100

; TELEFAX: 904-372-5800

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3543 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

Fax number: . (619)453-6991



TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US94-07902-27

Query Match 12.8%; Score 765.8; DB 6; Length 3543;  
Best Local Similarity 71.5%; Pred. No. 2.2e-161;  
Matches 1058; Conservative 0; Mismatches 397; Indels 24; Gaps 3;

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QY 2292 AATAAGCGAAAGGTTGTGAGTCTCTATGTTTACAGTAGTACGAAATAACGTTAAAAA 2351
DB 2072 AAACAGTACAAATAAATAATTAATACATTTTATGCAATCTCTATAAAAAACATTTTAAAT 2131
QY 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTTCTTATAGAATGTATGTCAGATG 2411
DB 2132 CAGAACTTACAGATTATGACATAGATCAAGCGCCCAATCTTGTGGAATGTATTTCTGAAG 2191
QY 2412 AACAAATCTCAGGAAATAATAATGTTTATGGGATGAATAAATACTGGCAAAACAACCTTA 2471
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QY 2646 ATGAGTCTAAATTAATAACCATATACAGTTTATCGAGTAAGAGGTTTGTGGGAAGTAGTA 2705
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QY 3240 TTCAAAACGCTGATCGACTGGTACAGTCGATTCCTTATGTATACCAATAATTGGTTACCGA 3299
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DB 3080 ATGCTCCAGGTATGAATATGATATATCTATAGAGTTGGATGACGAGTGGCAACAGCGC 3139
QY 3360 ATAATTTATATGATGACGAAATGTCTATACAAATGGTGACTTTTACCAAGGATTAACAG 3419
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QY 3420 GATGGCAGCAACAGAGAAATGCCCGGTACAAACAAATGGATGGAGCTTTCAGTATTAGTTC 3479
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QY 3720 CATTTATATAGATACATCGAGTTCGTTTGTATGCAAG 3758
DB 3500 CGTTTTATATCGAAAGCATTTGAATTAATTTTGCATGAACG 3538
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## RESULT 3

US-10-089-678-2  
; Sequence 2, Application US/10089678  
; Patent No. 6962977  
; GENERAL INFORMATION:  
; APPLICANT: ASANO, Shinichi  
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,  
; FILE REFERENCE: Q68821  
; CURRENT APPLICATION NUMBER: US/10/089, 678  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: JP 2000-236140  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 3504  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1)..(3501)  
; OTHER INFORMATION:  
US-10-089-678-2

Query Match 6.4%; Score 380.8; DB 3; Length 3504;  
Best Local Similarity 55.4%; Pred. No. 2.7e-75;  
Matches 881; Conservative 0; Mismatches 622; Indels 87; Gaps 4;

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QY 2221 ACCCGGTGAACGATCTGTTTACCAATTAACAAATAATTTACTAGATAGTGGTATT 2280
DB 1953 AGGAGGAGAGGTTTATGTAGATAAGTTTCGAACCTTATTCGGGTAAATGCAACATTTGAAGC 2012
QY 2281 GCTGTTTAACAATAAGCGAAAGGTTGTGAGTCCCTATGTTTACAGTAGTAGCAAAAA 2340
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Db 2013 AGAAGAAGACCTAGATGTGGCAAGAAAGCAGATGAATGCGTGTGTTTACGAGTAAAAAGA 2072  
Qy 2341 TAGGTTTAAAAATAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCCTATGAAATG 2400  
Db 2073 TGCCTTACAGACAAGGTGAACGGATTATCAAGTGAATCAAGCGGCAAACTTAGTAGAATG 2132  
Qy 2401 TATGTCAGATGAACAAAATCCTCAGGAAAAATAATATGTTATGGGATGAATAAACTGGC 2460  
Db 2133 CCTATCCGATGAGTTATACCCAAATGAAACCGAATGTTATGGGATGCGATGAAAGAGGC 2192  
Qy 2461 AAAACAACCTTAGTCAGTCTGCTAATCTACTCCAAAATGGAGACTTTTCTGGGAATCAT-- 2518  
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Db 2373 TCTCTATCAACAANTAGATGAATCACTTTTAAACCATATACAGATATAAATACTAAAGG 2432  
Qy 2689 GTTGTGGGAAGTAGTAAGATTTGAATTTAATGTTAAACAGTTACGGGAAAGAAATTGA 2748  
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Qy 2749 TGCATCATGAATGTTCCAAATGATTTGGCTATATGCGAGCTTAATCCTTTCATGTGGAGA 2808  
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Qy 2809 TTATCGCTGGAATCATGCTCAGTATGTCAGTATGTCAGCCAAAGGTATCTACACCAACATGS 2868  
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Qy 2869 ATATGCTCCCGATGATGTCATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCA 2928  
Db 2613 AGAAAATGGAATATGCTTCT----- 2634  
Qy 2929 CGATCGTCACTCAATTTGATTTTTCATATTGACACCGGAGATGATACAAATCAATGT 2988  
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Qy 2989 AGGTATTGATGCTTATTAATAATTTCTAATCCAGATGGATGCTACAGTACGGGAATCT 3048  
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Qy 3109 AAGAAATGGAACACACATGAGAGAAAACGTTGGGAACACACAGCCCTATGATCC 3168  
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Qy 3169 AGCAAAACAGGCTGTAGATGCTATTATTAATAATGAACAGAGTTACACTATCATATTAC 3228  
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Qy 3229 TTTTGA-----TCATATTCAAAACGCTGATCGACTGGTACAGTCCGATTCCTTATGTATA 3282  
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Qy 3343 ACGTATCATGCAAGGTTTAAATTTATATGATGACGAAATGTATCAACAAATGGTGACTT 3402  
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Db 3354 TGATACAGGTGTTTTATCTGTGATCAAACTAGCTATATCACAAAAACAGTGGAAATTAC 3413  
Qy 3673 CCCAGAAAAGTGCCTGTACCGATTGAAATAGGAGAAACCGAAGGTACATTTTATATAGA 3732  
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Qy 3733 TAGCATCGAGTTGCTTTGTATGCAAGGATA 3762  
Db 3474 AAGTGTAGAACTCGTGTTAGAAGAAGATA 3503

RESULT 4

US-10-089-678-3  
; Sequence 3, Application US/10089678  
; Patent No. 6962977  
; GENERAL INFORMATION:  
; APPLICANT: ASANO, Shinichi  
; TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN, A  
; FILE REFERENCE: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD  
; CURRENT APPLICATION NUMBER: US/10/089,678  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: JP 2000-236140  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: PCT/JP01/06660  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3690  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-10-089-678-3

Query Match 6.4%; Score 380.8; DB 3; Length 3690;  
Best Local Similarity 55.4%; Pred. No. 2,7e-75; Indels 87; Gaps 4;  
Matches 881; Conservative 0; Mismatches 622;

Qy 2221 ACGCGTGAACGATCTGTTTACCAATTAAACCAAAATTAATTTACTAGAAATAGGTGTTAT 2280  
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Qy 2281 GCTGTTTAAACAATAAGCGAAAAAGGTTGTGAGTCTGTGTTTACAGTAGTAGACGAAAAA 2340  
Db 2199 AGAAGAAGACCTAGATGTGGCAAGAAAAGCAGTAAATGSGCTTTGTTTACGAGTAAAAAAGA 2258  
Qy 2341 TAGCTTTAAAAATAGAAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCCTATAGAAATG 2400  
Db 2259 TGCCTTACAGACAGTGTACCGATTATCAGTGAATCAAGCGGCAAACTTAGTAGATAG 2318  
Qy 2401 TATGTCAGATGAACAAAATCCTCAGGAAAAATAATGTTTATGGGATGAAATAAACTGGC 2460  
Db 2319 CCTATCCGATGATTATATCCCAATGAAAAACGAATGTTTATGGGATGCAAGTGAAGAGGC 2378





|    |      |   |      |
|----|------|---|------|
| Db | 2995 | AAATGCGCAAGAAAACGTCGAGCATCAGAAAAACATATTTATGCGAGCAAGCAAGCCATT  | 3054 |
| Qy | 3185 | GATGCAATTATTTACAATGAACAAGAGTTACACTATCATATTAATTAG- - - - -TCAT | 3238 |
| Db | 3055 | GATCGTTTATTCGAGAGTATCAAGACCAAAAACCTTAATTTCTGGTGAGAAATGTCAGAT  | 3114 |
| Qy | 3239 | ATTCAAAACGCTGATCGACTGGTACAGTCCGATTCCCTATGTATACCATATTTGGTTACCG | 3298 |
| Db | 3115 | TTGTGGCAGCCCAAAACCTTGTACAGTCAATTCCTTACGTATATATGATGCGTTACCG    | 3174 |

Db  
3175 GAAATCCCTGGAATGAACATATACGAGTTTTACAGAGTTAAACAAATAGACTCCAAACAAACA 3234  
3399 AATGCTCCAGGATGAACTATGATGTATCAAGAGTTAAACGCGACGTATCATCGAAGGT 3355  
3399 AATGCTCCAGGATGAACTATGATGTATCAAGAGTTAAACGCGACGTATCATCGAAGGT 3355

|    |      |   |      |
|----|------|---|------|
| Qy | 3359 | TATAAATTATATGATGACGAAATGTCATAACAAATGGTGACTTTACACAAGGATTACAG   | 3411 |
| Db | 3235 | TGCAATTGTGTATCTTCAAAAACGCTATACCAAAATGGAGATTTTCGAAATGGATTAAAGT | 3294 |
| Qy | 3419 | GGATGGCAGCACACGGAATGCCGGGTACACAAATGGATCGAGCTTCAGTTAGTT        | 3478 |
| Db | 3295 | AATTGGAATGCAACATCAGATGTAATGTGCAACAACTAAGCGATACATCTGTCCTTGTC   | 3354 |
| Qy | 3479 | CTATCAAAATGGAGCGCGGGGTATCTCAAAACCTTCGATGCTCAAGATCATCATGGATAT  | 3538 |
| Db | 3355 | ATTCCAACTGGAAATCTCAAGTGTCAACANTTTACAGTTCAA CGGAATTTATAGNAT    | 3414 |
| Qy | 3539 | GTGTTACGTGTGATGTCCAAAAAAGAGACCTTGGAAAAAGGGTATGTAAACGATGATGGAT | 3598 |
| Db | 3415 | GTGTTACGTGTACACGCGAGAAAAAGGGAGTAGGAGACGGATATGTGTATCATCCCGTAT  | 3474 |
| Qy | 3599 | TGTAATGGAAAGCAGGAAACACTTAAAGTTTCACCTTCTTCGGAAGAAG             | 3644 |
| Db | 3475 | GGTGCAAAATCGACAGAAACACTCACATTTAATATATATGTGTATGATG             | 3520 |

RESULT 7  
 US-08-789-449-1  
 ; Sequence 1, Application US/08789449  
 ; Patent No. 5824878  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ohba, Michio  
 ; APPLICANT: Iwahana, Hidenori  
 ; APPLICANT: Sato, Reiichi  
 ; APPLICANT: Suzuki, No. 5824878ukazu  
 ; APPLICANT: Ogiwara, Katsutoshi  
 ; APPLICANT: Sakanaka, Kazunobu  
 ; APPLICANT: Hori, Hidetaki  
 ; APPLICANT: Asano, Shouji  
 ; APPLICANT: Kawasugi, Tadaaki  
 ; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: US  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/789,449  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/272,887  
 ; FILING DATE: 08-JUL-1994  
 ; APPLICATION NUMBER: US 07/915,203  
 ; FILING DATE: 23-JUL-1992  
 ; ATTORNEY/AGENT INFORMATION:

```

RESULT 7
US-08-789-449-1
; Sequence 1, Application US/08789449
; Patent No. 5824878
; GENERAL INFORMATION:
; APPLICANT: Ohba, Michio
; APPLICANT: Iwanana, Hidenori
; APPLICANT: Sato, Relichi
; APPLICANT: Suzuki, No. 5824878ukazu
; APPLICANT: Ogiwara, Katsutoshi
; APPLICANT: Sakanaka, Kazunobu
; APPLICANT: Hori, Hidetaki
; APPLICANT: Asano, Shouji
; APPLICANT: Kawasaki, Tadaaki
; TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,449
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,887
; FILING DATE: 08-JUL-1994
; APPLICATION NUMBER: US 07/915,203
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/K 301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: japonensis
; INDIVIDUAL ISOLATE: Buihui
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3636
; US-08-789-449-1

Query Match      6.0%; Score 358; DB 2; Length 3797;
Best Local Similarity 56.8%; Pred. No. 3.4e-70;
Matches 776; Conservative 0; Mismatches 530; Indels 60; Gaps 4;

QY 2297 GCGAAAGGTTGTGAGTCTCTATGTTTACAAAGTAGTACGAAATAACGTTAAATAATAGAA 2356
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DB 2254 GTAACGGATTTCAAGTCAATCAAGCGGCAAACTTAATAGAAATGCCCTATCCGATGAGTTA 2313
QY 2417 AATCCTCAGGAAAAAATAATGTTATGGATGAATAAACTGGCAAAAACAACTTAGTCAG 2476
DB 2314 TACCCAAATGMAAACGATGTTATGGGATGCGTGAAGGCGGAAACGACTTGTTCAG 2373
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DB 2494 TTGACAAGTGGGAGAGATTTGATACAGAAACATATCCAACTGATCTCTATCAACAAATA 2553
QY 2645 GATGAGTCTAAATTTAAACCATATACACGTTATCGAGTAAGAGGGTTTGTGGGAAGTAGT 2704
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QY 2705 AAGATTTGAAATTAATGTAACACGTTACCGGAAAGAAATTCATCTATCATGAATGTT 2764
DB 2614 CAAGATTTAGAGATTAATTAATACGTCTACGCGGCAAAATCAAAATCGTCAAAAATGTACCA 2673
QY 2765 CCAAAATGATTGGCCCTATATGACGCTTAATCCTTTCAATGAGGATTAATCGCTGTAATCA 2824
DB 2674 GATATCTCTTGCCAGATGTACGCCCTGTCAATTTCTTGTGGTGGATCGATCGCTCGAT 2733
QY 2825 TCGTCTCAGTATGTGACCAAGGGTATCCCTPACACCAACAGATGATATGCTCCCGATATG 2884
DB 2734 GAACACAGATGTATGACGCGGAATTTAGCACTCGAAAAACAATGGAGAAAAATGAAATATG 2793
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DB 2794 TCTTCT-----GATTCCTCAATGTTT-----GATTCCTCAATGTTT 2814
QY 2945 GATTTTTCATATTCACACCGGAGAGTAGATACAAATACAAATGTAGTATTTGATGCTTA 3004
DB 2815 TCCTTCCATATTCATACGGGTGAATAGATTTGAATGAAAAATACAGAAATTTGGATCGTA 2874
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QY 3005 TTAAAAATTTCTAATCCAGATGGATACGCTACAGTAGGGAATCTTAGAAGTCAATTGAAGAA 3064
DB 2875 TTTAAATTTCCGACAAACAAATAGGAACGCAACACTAGGAAATCTTGAATTTGTAGAGAG 2934
QY 3065 GGACCACTAAACAGGTGAAGCAATGGCACATGTGAACAAAGAAAGAAAGAAATGGAACAA 3124
DB 2935 GGGCCATTTGTAGGGGAAACATTAAGATGGGCCCAACAAAGAAACAAATGGAAGAC 2994
QY 3125 CACATGGAGAAAAAACGTTGGGAAACACAAACAAAGCCTATGATCCAGCAAAACAGGCTGTA 3184
DB 2995 AAAATGGCAAGAAACGTCGAGCATCAGAAAAACATATATGACAGCAAAACGACCAT 3054
QY 3185 GATGATTTATTAACAAATGAACAGAGTTACATATCATATTAATTTTGA-----TCAT 3238
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QY 3239 ATTCAAAACGCTGATCGACTGGTACAGTCGATCCCTATGATATACCAATTTGGTTACCG 3298
DB 3115 TTGTTGGCAGCCCAAAACCTTTGACAGTCCATTCCTTACGTATATAATGATGCGTTACCG 3174
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QY 3359 TATAATTTATATGATGACGAAATGTATATAACAAATGTGTGACTTTTACAAAGGATTAACAG 3418
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QY 3599 TGTAAATGMAAGCAGGAAACACTTAAGTTCACTTCTTCGGAAGAG 3644
DB 3475 GGTGCAAAATCAGACAGAAACACTCACTTAATATATGTGATGATG 3520
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## RESULT 8

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US-07-876-280-29
; Sequence 29, Application US/07876280
; Patent No. 5262158
; GENERAL INFORMATION:
; APPLICANT: Payne, Raymond J.C.
; APPLICANT: Cannon, Raymond J.C.
; APPLICANT: Bagley, Angela L.
; TITLE OF INVENTION: NO. 5262158el Bacillus thuringiensis Isolates for
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,280
; FILING DATE: 19920430
; CLASSIFICATION: 514
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; CORRESPONDENCE ADDRESS:

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/ ADDRESS: Roman Saliwanchik
/ STREET: 2421 N.W. 41st Street, Ste A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/812,180A
/ FILING DATE: 19920102
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, Roman
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3471 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus thuringiensis
/ STRAIN: kumamotoensis
/ INDIVIDUAL ISOLATE: PS50C
/ IMMEDIATE SOURCE:
/ LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF LUIS
/ CLONE: 50C
/
/ US-07-812-180A-1
/
/ Query Match 5.3%; Score 314.6; DB 2; Length 3471;
/ Best Local Similarity 55.7%; Pred. No. 1.7e-60;
/ Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps 8;
/
/ QY 2292 ATAAGCGGAAAAGGTTGTGAGTCTATGTTTCAAGTAGTAGTACGAAAATACGTTTAAAAA 2351
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/ DB 2015 AAGCGGGAAGAAGCAGTGAATGCTTGTGTAC---GAATACAAAAGATGGCTTACGAC 2071
/
/ QY 2352 TAGAACGACAGATTATGAATAGATCAAGCGGCCATTTCTATAGAAATGTATGTCTAGATG 2411
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/ DB 2072 CAGGTGTACGGATTATGAAGTAAATCAAGCGGCAAACTTAGTGGAAATGCCATCGGATG 2131
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/ QY 2412 AACAAATCCTCAGGAAAAATAATGTTATGGGATGAAATATAAACTGGCAAAACAACTTAA 2471
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/ DB 2132 ATTTATATCCAAATGAANAACGATTGTTATTTGATCGCGTGAGAGAGGCAAAACGCTCA 2191
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/ QY 2472 GTCAGTCTCGTAACTCTCCAAAATGGAGACTTTTCTGGG-----AATGATT 2519
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/ DB 2192 GTGGGCGAGTAACTTACTACAGATCCAGATTCCAGATTCCAAAGAGATAAAACGGAGAAAATGGAT 2251
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/ QY 2520 GGACATTCGGTAAATGATATATCATAGGATCCAAATATCCTATTTTAAAGGAAATTTTC 2579
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/ DB 2252 GGGCGGCAAGTACGGGAAATTTGAGATTGTAGAGGGGATGCTGTATTTAAAGGACGTTATC 2311
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/ QY 2580 TACAGATGGGTGAGCAGCAGAGATATATATGGAATCTATTTTCCAACTTATCTGTCAAA 2639
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/ DB 2312 TAGCGCTACAGGTGCACGAGAAATTTGATACGGAACGATCCAAAGTATCTGTATCAAA 2371
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/ QY 2640 AAATAGATGAGTCTAAATTAACCAATATACAGTTATCGAGTAAGAGGGTTTGTGGGAA 2699
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/ DB 2372 AAGTAGAGGAAGGTGTATTAACCAATATACAGATATAGACTGAGAGGGGTTTGTGGGAA 2431
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/ QY 2700 GTAGTAAAGATTGAAATTAATGGTTAACACAGCTTACGGGAAAGAAATTTAGTGTATCATGA 2759
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/ 2432 GTAGTCAAGGATTAGAAAATTTATACGATACGTAC---CAAACGAATCGAATTTGTTAAAGA 2488
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/ QY 2760 ATGTTCCAAATGATTTGGCCTATATGCAGCCTAATCTTCTATGTGGAGATTATCGCTGTG 2819
/ |||||||
/ DB 2489 ATGTACCAAGATGATTTATTGCCA-----GATGATCTCTCTGTA 2526
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/ QY 2820 AATCATCGTCTCAGTATGTGAGCCAAAGGGTATCTTACCAACCAAGATGATATGCTCCCG 2879
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/ DB 2527 AACTCTGATGGCAGTAT-----CAATCGATGCAGCAACAAAGATGTGTAATAGCCGT 2580
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/ QY 2880 ATATGATGCAATGCCCGCAAAATATAGATAGAAACATGTGAAGTGTCCAGATCGTCATC 2939
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/ QY 2940 CATTTTGAATTTTCAATTTGACACCGGAGAAAGTAGATACAAATACAAATGTAGGTATTGATG 2999
/ |||||||
/ DB 2615 AGTTCTCGCTCCCTATCGATATAGGAGAGCTGGATTACAATGAAATGCAGGAATATGGG 2674
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/ QY 3000 TCTTATTAATAATTTCTAATCCAGATGGATAGCTACAGTAGGGGAATCTAGAAATGATG 3059
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/ DB 2675 TTGGATTTAAGATTTACGGACCCAGAGGGATACGCAACACTTTGGAATCTTGAATTAGTGG 2734
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/ QY 3060 AAGAAGGACCACTAACAGGTGAAGCATTTGGGCACATGTGAAACAAAGGAAAGAAATGGA 3119
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/ DB 2735 AAGAGGACCTTTTGTACGAGAGACGATTTAGAGCGCTTGCAAAGAGAAAGAAACAGTGA 2794
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/ QY 3120 AACAAACATATGGAGAAAAACGTTGGGAAACACAACAAAGCCCTATGATCCAGCAAAACAGG 3179
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/ DB 2795 AGATTTCAATGACAAGAAGACGTTGAAGAGACAGATAGAGATACATGGCATCGAAACAG 2854
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/ QY 3180 CTGTAGATGCATTATTTACAAATGAACAAAGAGTTACACTATCATATTTACTTTAGA----- 3234
/ |||||||
/ DB 2855 CGGTAGATCGTTTATATCCGATTTATCAGGATCAACAACTGAATCCTGATGTAGAGATTA 2914
/
/ QY 3235 -TCATATTCAAAACGCTGATCGACTGGTACAGTCCGATTTCCCTATGTATACCAATATGTT 3293
/ |||||||
/ DB 2915 CAGATCTTACTGCGGCTCAAGATCTGATACAGTCCATTTCTTACGTATATAACGAATGT 2974
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/ QY 3294 TACCGAATGCTCCAGGTATGAATGATGATATATCAAGAGTTAAACGCAAGCTTCATGTC 3353
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/ DB 2975 TCCAGAAAATACACAGGGATGAATATACGAAGTTTACAGAATTAACAGATCGACTCCAAC 3034
/
/ QY 3354 AAGGTTTAAATTTATATGATGCAAGAAATGTATACAAATGCTGCTGCTGCTTACACAGAT 3413
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/ DB 3035 AAGCGTGGAAATTTGTATGATCAGCGAAATGCCATACCAATGGTGTGATTTTCGAAATGGGT 3094
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/ QY 3414 TACAGGGATGGCAGCAACAGGAAATGCGCGGTACAAACAAATGGATGGAGCTTCAGTAT 3473
/ |||||||
/ DB 3095 TAAGTAAATGGAAATGCAACGCTGCGGTAGAGTACAAACAAATCAATCATATCTGTCTC 3154
/
/ QY 3474 TAGTTCTATAAATTTGGAGCGCGGGGTATCTCAAAACTTGCATGCTCAAGATCATCATG 3533
/ |||||||
/ DB 3155 TTGTGATTTCCAAACTGGGATGAACAAAGTTTCAACACAGTTTACAGTTCAACCGGAATCAA 3214
/
/ QY 3534 GATATGTGTAGCTGTGATTGCCAAAAAAGAGGACCTGGAAAAAGGATGTAAACGATGA 3593
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/ DB 3215 GATATGTATTACAGTTTACTGCAAGAAAGAGGGGTAGGAAATGGATATGTAAGTATTC 3274
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/ QY 3594 TCGATTGTAAATGGAAGCAGGAAACACTTAAAGTTCACTTCTTTCGCG----- 3638
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/ DB 3275 GTGATGGTGGAAATCAATCAGAAAACGCTTACTTTTGTAGCAAGCGGATTTATGATACAAATG 3334
/
/ QY 3639 -----AAGAAGGATATATGACAAAAACAGTAGAGGTATTTCCAGAAAGTG 3683
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/ DB 3335 GTGTGTATAATGACCAACCGGCTATATCACAAAAAACAGTGACATTCATCCCGTATACAG 3394
/
/ QY 3684 ATCGTGTACGGATTGAAATAGAGAAACCGAAGGTACATTTTATATAGATAGCATCGACT 3743
/ |||||||
/ DB 3395 ATCAAAATGGGATTGAAATTAAGTGAACAGAGGTACGTTCTTATATAGAAAGTGTAGAAT 3454
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/ QY 3744 TCGTT 3748
/ |||||||
/ DB 3455 TGATTT 3459
/ |||||||
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RESULT 10  
US-08-315-468-1  
; Sequence 1, Application US/08315468  
; Patent No. 5554534  
; GENERAL INFORMATION:  
; APPLICANT: Michaels, Tracy Ellis  
; APPLICANT: Fonceerrada, Luis  
; APPLICANT: Narva, Kenneth E.  
; TITLE OF INVENTION: Process for Controlling Scarab Pests  
; TITLE OF INVENTION: with Bacillus thuringiensis Isolates  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/315,468  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/014,941  
; FILING DATE: 01 FEB 1993  
; APPLICATION NUMBER: 07/828,430  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/808,316  
; FILING DATE: 16-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: MA73.C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; STRAIN: kumamotoensis  
; INDIVIDUAL ISOLATE: PS50C  
; IMMEDIATE SOURCE:  
; LIBRARY: LAMBDA GEM (TM) - 11 LIBRARY OF LUIS  
; LIBRARY: FONCERRADA  
; CLONE: 50C(a)  
US-08-315-468-1

Query Match 5.3%; Score 314.6; DB 2; Length 3471;  
Best Local Similarity 55.7%; Pred. No. 1.7e-60;  
Matches 838; Conservative 0; Mismatches 559; Indels 108; Gaps 8;  
Qy 2292 AATAAGCGAAAGGTTGTGAGTCTTACAGTACGAAAAATACGTTAAAA 2351  
Db 2015 AAGCGGGAAGAAGCGATGAACTGTTTAC---GAATACAAAGATGGCTTACGAC 2071  
Qy 2352 TAGAAACGACAGATTATGAATAGATCAAGCGGCCATTCTATAGAAATGATGTCAGATG 2411

Db 2072 CAGGTGTAACGGATTATAGTAATAACAAGCGCAAACTTAGTGAATGCTATCGGATG 2131  
Qy 2412 AACAAAATCTCAGGAAAAAATAATGTTATGGGATGAATAAAACTGGCAAAACAACCTTA 2471  
Db 2132 ATTTATATCCAAATGAATAACGATTGTTATTTGATCGGTGAGAGAGCAAAACGCCCTCA 2191  
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Db 2252 GGGCGGCAAGTACGGGAATTTGAGATTGTAGAAAGGATGCTGTATTTTAAAGGAGCTTATC 2311  
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Db 2432 GTAGTCAAGGATTAGAAATTTATACGATAGCTCAC---CAACGAATCGAATTTGTAAGA 2488  
Qy 2760 ATGTTCCAAATGATTTGGGCTATATGACGCTTAATCCTTCATGTGGAGATTTATGCGTGTG 2819  
Db 2489 ATGTACCAGATGATTTATTGCCA-----GATGTATCTCTGTGTA 2526  
Qy 2820 AATCATCGTCTCAGTATGTGAGCCAAAGGTTATCTACACCAAGATGATATGCTCCCG 2879  
Db 2527 AACTCTGATGGCAGTAT-----CAATCGATGAGGAAACAAAGTATGTAATAGCCGT 2580  
Qy 2880 ATATGTATGATGATGCGCCGCAAAATATAGATAGAAAGCATGTGAAGTGTGACGATCGTCATC 2939  
Db 2581 TTAGAGGAGAAACCGT-----TCTGGTGTGCATG 2614  
Qy 2940 CATTTGATTTTCAATTTGACACCGGAGAGTAGATACAAATACAAATGTATAGGTATTTGATG 2999  
Db 2615 AGTTCTCGTCTCCCTATCGATATAGGAGAGCTGGATTACAAATGAATAATGCAAGGAATATGGG 2674  
Qy 3000 TCTTTTAAAAATTTCTTAATCCAGATGGATGAGTACGCTACAGTGGGAATCTAGAGTCAATG 3059  
Db 2675 TTGGATTTAGATTACGACCCAGAGGATACCAACACTTGGAAATCTTTGAATTTAGTCG 2734  
Qy 3060 AAGAGGACCACTAAACAGGTGAAGCATTTGGCAGCATGTGAAACAAAGAGAAAGAAATGGA 3119  
Db 2735 AAGAGGACCTTTGTTCAGGAGAGCGCATTAGAGCGCTTGCNAAGAGAAGAACACACAGTGA 2794  
Qy 3120 AACACACATGGAGAAAAACGTTGGGAAACACAAACAGCTTATGATCCAGCAAAACAGG 3179  
Db 2795 AGATTCAAATGACAGAAGACGTTGAAGAGACAGATAGAAAGATACATGGCATCGCAAAACAG 2854  
Qy 3180 CTGTAGATGCATTTTAAATTAACAAAGAGTTACACTATCATATATCTTTTGA----- 3234  
Db 2855 CGGTAGATCGTTTATATCGGATTATCAGGATCAACAACTGAATCTCTGTATGATGAGATTA 2914  
Qy 3235 -TCATATTCAAAACCGTGTGACCTGGTACAGTCGATTCCCTATGTATATACATAAATTTGGT 3293  
Db 2915 CAGATCTTACTCGGGCTCAAGATCTGATACAGTCCATTCTTACGTATATTAACGAATGT 2974  
Qy 3294 TACCGAATGCTCAGGTATGAACATGATGATATATCAAGATTAAACGACGCTATCATGTC 3353  
Db 2975 TCCAGAAATACACAGGATGAACATATCAAGTTTACAGAAATTAACAGATCGCACTCCAAC 3034  
Qy 3354 AAGTTTATATTTATATGATGACGAAATGTCTATACAAATGGTGTACTTTTACACAGGAT 3413  
Db 3035 AAGCGTGGAAATTTGTATGATCAGCGAAATGCCATACCAATGGTGTATTTTCGAAATGGGT 3094  
Qy 3414 TACAGGGATGGACGCAACAGGAAATGCGCGGTGACAAACAAATGGATGGAGCTTCAGTAT 3473  
Db 3095 TAAGTAATTTGGAATGCAACGCCCTGGCGGTAGAGATGACAAATCAATCATATCATCTGTCTC 3154



|    |      |   |      |
|----|------|---|------|
| Qy | 3180 | CTGTAGATGCATTATTTACAAATCGAACAGAGTTTACACTATCATATTTACTTTAGA-----  | 3234 |
| Db | 2985 | CGGTAGATCGTTTATATGCCGATTTATCAGGATCAACAACCTGAATCCTGATGTAGAGATTA  | 2914 |
| Qy | 3235 | -TCATATTTCAAAACGCTGATCGACTGGTACAGTCCGATTCCTATGTATATCCATATTTGGT  | 3293 |
| Db | 2915 | CAGATCTTACTCGCGCTCAAGATCTGATACAGTCCAATCTCTTACGTATATAACGAAATGT   | 2974 |
| Qy | 3294 | TACCGAATGCTCCAGGTATGAACATATGATGTATATCAAGAGTTTAAACGCAAGTATCATGC  | 3353 |
| Db | 2975 | TCCCAGAAATACAGGGATGACATATACGAAGTTTACAGAAATTAACAGATCGACTCCAAC    | 3034 |
| Qy | 3354 | AAGTTTAAATTTATATGATGCACGAAATGTCTAAACAAATGGTGTGACTTTTACACAAGGAT  | 3413 |
| Db | 3035 | AAGCGTGGAAATTTGTATGATCAGCGAAATGCCATACCAAATGGTGTGATTTTCGAAATCGGT | 3094 |
| Qy | 3414 | TACAGGGATGGCAGCAACAGGAAATGCCGGGTACAACAANTGGATGGAGCTTCAGTAT      | 3473 |
| Db | 3095 | TAAGTAANTGGAATGCACACGCTGGCTGAGAGTACAAACAATCAATCATACATCTGTGCC    | 3154 |
| Qy | 3474 | TAGTTCTATCAAAATTTGGAGCGCGGGGTATCTCAAAACTTGTGCATGCTCAAGATCATCATG | 3533 |
| Db | 3155 | TTGTGATTCCAAACCTGGATGAAACAAGTTTCACAACAGTTTACAGTTCAACCGAATCAAA   | 3214 |
| Qy | 3534 | GATATGTTGTACGTGTGATTTGCCAAAAAAGAGCACTGGAAAAGGTATGTAAACGATGA     | 3593 |
| Db | 3215 | GATATGTATTACGAGTTTACTGCAAGAAAAGAGGGGTAGGAAATGGATATGTAAGTATTC    | 3274 |
| Qy | 3594 | TGGATTCTTAATGGAAAACAGAGAAACACTTAAGTTTCAGTTCTTCG-----            | 3638 |
| Db | 3275 | GTGATGTGGAAATCAATCAGAAACGTTTACTTTTGTGCAAGGATTTGATACAATG         | 3334 |
| Qy | 3639 | -----AAGAAGGATATATGACAAAAACAGTAGAGGTATTTCCCAAGAAAGTG            | 3683 |
| Db | 3335 | GTGTGTATAATAGCAAAACCGGCTATATCAAAAAACAGTGAACATTCATCCCGTATACAG    | 3394 |
| Qy | 3684 | ATCGTGTACGGATTTGAAATAGGAGAACCGAAGTACATTTTATATAGATAGCATCGAGT     | 3743 |
| Db | 3395 | ATCAATGTGATTTGAAATTAAGTGAACAGAAAGTACGTTCTATATAGAAGTGTAGAAT      | 3454 |
| Qy | 3744 | TGCTTT  | 3748 |
| Db | 3455 | TGATT   | 3459 |

RESULT 12

|  |
|--|
| US-09-001-982-11                                 |
| ; Sequence 11, Application US/09001982           |
| ; Patent No. 6204246                             |
| ; GENERAL INFORMATION:                           |
| ; APPLICANT: Bosch, Hendrick J.                  |
| ; APPLICANT: Stiekema, Willem J.                 |
| ; TITLE OF INVENTION: Hybrid Toxin               |
| ; NUMBER OF SEQUENCES: 15                        |
| ; CORRESPONDENCE ADDRESS:                        |
| ; ADDRESSEE: No. 6204246artis Corporation        |
| ; STREET: 3054 Cornwallis Road                   |
| ; CITY: Research Triangle Park                   |
| ; STATE: NC                                      |
| ; COUNTRY: USA                                   |
| ; ZIP: 27709                                     |
| ; COMPUTER READABLE FORM:                        |
| ; MEDIUM TYPE: Floppy disk                       |
| ; COMPUTER: IBM PC compatible                    |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS                |
| ; SOFTWARE: Patentin Release #1.0, Version #1.30 |
| ; CURRENT APPLICATION DATA:                      |
| ; APPLICATION NUMBER: US/09/001.982              |
| ; FILING DATE:                                   |
| ; CLASSIFICATION:                                |
| ; PRIORITY APPLICATION DATA:                     |
| ; APPLICATION NUMBER: US 08/602,737              |

Db 828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATACCCAAATAGAAACAGA 887  
QY 1097 TGTAGAGTTGACTAGGGAATTTATACAGATCAGTGGGATATTTCATCGGAACTTATAG 1156  
Db 888 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCATTTGGTTTGTACATCGTAGTCT 947  
QY 1157 TTGGTTACGGAATGGCCCTAATACTTTTAAATGGTTAGAGGCTTAATGGAACACGGGACC 1216  
Db 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAATAGA-----GCTAAATTTCTCAGATTTAGA 1001  
QY 1217 TGGTTTGTAGTTAGTCTAGCAAAATAGGTATATATATAGTATGTTTCGAGATATT 1276  
Db 1002 AAATGCAATACCTAAATCTCTAG-ACCGTCTTGGTTTTTAAATAATATGATTTATCTACTG 1060  
QY 1277 TGGCGGTGGGTAGGAATCGTCAATTAATGAAGACTACACAAAGGGTAACGGTATTTTTCA 1336  
Db 1061 GTTCACCTTACATTTGCCGTTAGCCCAAGTACTGATAGAGGGGTATCG-----TATGG 1115  
QY 1337 ACGTATGTCTGGAACCTACGAGTAAATGATCTACGTAAATATTTGATTTTCAGAAATGCCGATG 1396  
Db 1116 AAGTCGAGATCGAAATTTCCCTGCTAAATTCACAAATTTATTTACTGAACTAATCTCTGGACA 1175  
QY 1397 ATATAAAATTTACTTTAGTCTATCATGAACCTAGTAGGAGACTACCGCTAGACCAGA 1456  
Db 1176 ACATACGACTGCTACACAAACTATTTTAGGGCGAATAATATTTAGAGTAGATTTCTCAAG- 1234  
QY 1457 GTATCGTGTTCAAAGCCAGATTTTCGTAGGGTAGGGGACCTGATTTAAATTTATGATGC 1516  
Db 1235 --CTTGTAAATTAATGATACCACATATGAGTGAATAGGGCGGTATTTTATCATGATGC 1292  
QY 1517 AGGTAATAATGGGCTTAAGCAGGATGACAAATGGAATCTACGTTCCCACTTGTTGCACTC 1576  
Db 1293 GAGTGAAGGTTCTCAAGATCCGTG-----TACGAGGGGTATATTTCGAA 1336  
QY 1577 TAATGTGTAGAGGACCTCTCATAGATTATCAAAATCGGCATGTGTTGTATATGAA 1636  
Db 1337 CAACCTGGGATAGATAACCC-----TAGAGTTCAAAATATAAACACTATTTTACCTGGAGA 1391  
QY 1637 CTCACAGATTAAAGTATATGTTGGACACATACAAAGTTTAAACGTAAGAAATATAATGCA 1696  
Db 1392 AAATTCAGATATCCCAATCCAGAGACTATCTCATATATTAAGCACAACTAATATT 1451  
QY 1697 AGCAATCAAAATPACAAATACCGCGGTGAAGATTTATACCTTCAAAATTTATCTGC 1756  
Db 1452 AACAGGAGGACTTTAGACAAGTAGCATCTAATCCCGTTCATCTTTAGTAATGATGGTTG 1511  
QY 1757 TAATGCTTATACCTATGTAATAAGGCACTCAT- -CAGTGGGATTTAATCCGTTTT 1814  
Db 1512 GACATATAAAGTCTGGCTCGTAACCAATACCATTAATCCAGATAGAATTACAGATACC 1571  
QY 1815 TTAAGAACAAAATCAGAGTATAACGAGTTTATGCAAGGTGGCGGAATTAGATTGATTAT 1874  
Db 1572 TTTAGTGAAGGATTTAGAGTTTGGGGGGCACTCTGTCAATTACAGGACCGAATTAC 1631  
QY 1875 AATAACAAACTCGAGA CAAAGTTACCGTAITTCGTTTTCGTTATGCTGCGAGATAAGCT 1934  
Db 1632 AGGAGGGGATATCCTTCGAAGAAATACCTTTGGTGATTTTGTATCTCTCAAGTCAATAT 1691  
QY 1935 GCTTTCTTTAGTGTATCTTTTATCCAGGAGTTGGGTTCAATCGTTTGTATCGCTT 1994  
Db 1692 TAATTCACCAAT- -TACCCAAGATACCGTTTAAAGATTTTCGTTACGTTCCAGTAGGATG 1750  
QY 1995 GAAAAATCTTACTCTGGAAATTAAGCATTTTAAAAATATAGTGAATTTAAATTCGCTGAA 2054  
Db 1751 CACGAGTTATAGTATTAAACAGGACCGCATCCACAGGATGGGAGGCCAAGTTAGTGTA 1810  
QY 2055 ATTATCACACCTCCATTTACTAGTTTCAACATTTACAGATGATGTGAGATGCAAGCGAAT 2114  
Db 1811 AT-----ATGCTCTTTCAGAAAACCTATGGAATAGGGAGAACTTTAACTCT 1857  
QY 2115 AGTTTTCAATCAGATGTAAACGGTGTCTTCGACAAAAATGCAATTTCTCCCAAGTAATACA 2174

Db 1858 AG--AACATTTAGATATATACCGATTTTAGTAATCTCTTTTCAATTTAGAGCTAATCCAGATA 1915  
QY 2175 ACAACTTTAGATATATAGGGAGAACGGACCTTAGAAAAAACAAGAACCGGTGAACGAT 2234  
Db 1916 TAATTTGGGTAAGTGAAACAACCTCTATTGTTGGTGCAGGTTCTATTAGTAGCGGTGAACTTT 1975  
QY 2235 CTGTTTACCAATTAACAAATAATTTACTAGTAATAGGTGGTATGCTGTTTAA- -CA 2291  
Db 1976 ATATAGATAAAATTTGAAATTTATTTAGCAGATGCAACATTTTGAACGAGAAATCTGATTTAG 2035  
QY 2292 AATAAGCGAAAGGTTGTGAGTCTCTATGTTTACAAGTAGTACGAAAAATACGTTAAAAA 2351  
Db 2036 AAAGAGCAAAAGGCGGTGAATGCCCTGTTTACTTCTTCCATCAATCGGTTTAAANA 2095  
QY 2352 TAGAAACGACAGATTATGAAATAGATCAAGCGGCCATTTCTATAGAAATGTTATGTCAGATG 2411  
Db 2096 CCGATGTGACCGATTATCATATTGATCAAGTATCCAATTTAGTGGATTGTTTATCAGATG 2155  
QY 2412 AACAAAATCCTCAGGAAAAAATAATGTTATGGGATGAAATTAACCTGGCAAAAACAATTA 2471  
Db 2156 AATTTTGTCTGGATGAAAAAGCGAGAAATTTGCCGAGAAAAGTCAAAACATGCGAAGCGACTCA 2215  
QY 2472 GTCAGTCTGTAATCTACTCCAATAATGAGACTTTTCTGGGAATGATTTGGACATTCGGTA 2531  
Db 2216 GTGATGAGCGGAATTTACTTCAAGATCCAACTTCAGAGGGATCAATAGACAAACAGACC 2275  
QY 2532 ATGATATTATCATAGGATCCAATAATCTCTATTTTAAAGGAAAAATTTCTACAGATGCGGTG 2591  
Db 2276 GTGGCTGGAGGAGTAGTACAGATATTACCATCCAAGGAGGAGATGACGTATTTCAAAGAGA 2335  
QY 2592 GAGCAGGAGACATATATGGAACCT- ------ATTTCCAACTTATATCTGTCAAAAA 2642  
Db 2336 ATTACGTCACACTACCGGTGTACCGTTGATGAGTGTCTATCCAACGTATTTATATCAGAAA 2395  
QY 2643 TAGATGAGTCTAAATTTAAAAACCATATACAGCTTATCGAGTAAGAGGTTTGTGGGAAGTA 2702  
Db 2396 TAGATGAGTCGAAATTTAAAGCTTATACCGTTTATGAAATTAAGAGGTTATATCGAAGATA 2455  
QY 2703 GTAAAGATTTGAAATTAATGTTGTAACACGTTAGCGGAAAAAGAAATTTGATGCTATCATGAATG 2762  
Db 2456 GTCAAGACTTAGAAATCTATTGATCCGTAC- -AATGCAAAAACACGAATATGATAATG 2512  
QY 2763 TTCCAAATGATTTGGCCCTATATGAGCCTTAATCTTCAATGTGGAGATTATCGCTGTGAT 2822  
Db 2513 TGCCAGGACCGGTTTCTTATGGCCGCTTTTCAGCCCAAGTCCAAATCGSAAAGTTGGAG 2572  
QY 2823 CATCGTCTCAGTATGTGAGCCAAAGGTTATCCTACACCAACAGATGATGCTCCCGATA 2882  
Db 2573 AACCGAATCGATGG- ------CGCCACACCTTGAATGGAATCTCTGATC 2614  
QY 2883 TGTATGCAATGCCCGCAAAATATAGATAGAAAGCATGTGAAGTGTCCAGATCGTCATCCAT 2942  
Db 2615 TAGATTGTTCTTCGACAGACGGGAAAAA-----TGTGCACATCATTTCCCATCAT 2665  
QY 2943 TTGATTTTCATATTGACACCGGAGAGTAGATACAATACAATGATAGTATTGATGCT 3002  
Db 2666 TCACCTTGGATTTGATGTTGGATGACAGACTTAAATGAGGACTTAGGATGATGGGTA 2725  
QY 3003 TATTAATAATTTCTAATCCAGATGATACGCTACAGTAGGGAATCTAGAAAGTCATTGAAAG 3062  
Db 2726 TATTCAAGATTAAAGACGCAAGATGCCATGCAAGACTAGGGAAATCTAGAGTTTCTCGAAG 2785  
QY 3063 AAGGACCACTAA CAGGTGAAGCATTTGGCACATGTGAAACAAAAGAAAAAGAAATGGAAC 3122  
Db 2786 AGAAACCATTTATTAGGGGAAGCCTAGCTCGTGTGAAAAGAGCGGAGAAAGTGGAGAG 2845  
QY 3123 AACACATGGAGAAAAA CTTGGGAAAACACACAGCCTATGATCCAGCAAAACAGGCTG 3182  
Db 2846 ACANAACGAGAGAAACTGCGAGTTGGAAAACAAATATTTGTTTATAAAGAGGAAAAAGATCTG 2905  
QY 3183 TAGATGCAATTTTAAATAATGAAACAAG- ------GTTACACTATCATATTTACTTTAGATC 3236  
Db 2906 TAGATGCTTTATTGTTAAACTCTCAATATGATAGATTACAAGTGGATACGACATCGCGA 2965



QY 3237 ATATTCAAACGCTGATCGACTGGTACAGTCGATTCCCTATGTATATACCATTAATTGGTTAC 3296  
| | | | |  
Db 2966 TGATTCATCGGCAGATAAAGCGCTTCATAGAAATCCGGGAAGCATATCTCCAGAGTTGT 3025  
QY 3297 CGAATGCTCCAGGTATGAATCATATGATATATCAAGAGTTTAAACGCAAGTATCATGCAAG 3356  
Db 3026 CTGTGATTCAGAGTGTCAATCGGCCATTTTCGAAGAATTAGAGGACGTATTTTACAG 3085  
QY 3357 GTTATATTTATATGATGCGAGCAATGCTATACAAATGTGACTTTACACAGGATTAC 3416  
| | | | |  
Db 3086 CGTATTCCTTATATGATGCGAGAAATGTCAATTAATAATGCGATTTCAATAATGGCTTAT 3145  
QY 3417 AGGATGCGACGCAACAGGAAATCCCGCGGTACAA---CAATGGATGGAGCTTCAGTAT 3473  
| | | | |  
Db 3146 TATGCTGGAACGTGAAGGTCATGTAGATGTAGAGAGCAAAACACCCGTTCCGTCC 3205  
QY 3474 TAGTTCTATCAAAATGGAGCGCGGGGTATCTCAAAATCTTGCAATGCTCAAGATCATCATG 3533  
Db 3206 TTGTTATCCAGAAATGGAGGACAGAGTGTCAACAAGAGTTCTGTCTGTCAGGTCGTG 3265  
QY 3534 GATATGTTTACGTGATTTGCCAAAAGAGAGGACCTGAAAAGGATATGTAACGATGA 3593  
| | | | |  
Db 3266 GCTATATCCTTCGTGTCAACGATATATAAGAGGATATGAGAGGGCTGCGTAACGATCC 3325  
QY 3594 TGGATTGTAATGGAAGCAGAAACACTTAAAGTTCACTTCTTTCGGAAGAG 3644  
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Db 3326 ATGATCGAGACNATACAGACGACTGAATTCAGCAACTGTGTAGAAG 3376

## RESULT 13

US-09-668-650-11

Sequence 11, Application US/09668650

Patent No. 6780408

GENERAL INFORMATION:

APPLICANT: Bosch, Hendrick J.

Stiekema, Willem J.

TITLE OF INVENTION: Hybrid Toxin

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6780408artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/668,650

FILING DATE: 22-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/001,982

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 08/602,737

FILING DATE: 21-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3726 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3726  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-668-650-11

Query Match 5.2%; Score 308.2; DB 3; Length 3726;  
Best Local Similarity 48.0%; Pred. No. 4.6e-59;  
Matches 1607; Conservative 0; Mismatches 1588; Indels 156; Gaps 19;

QY 323 AATTTGGGAATCAGTCCGAAACGATACCAAGTATTTGGGATATAATCTTATAGAGTTTGTGAT 382  
| | | | |  
Db 153 AATAGSCGATGCAGCAAAAGAGCAGTATCTATTGGGACAAACCATAGTCTCTCTTATCAC 212  
QY 383 AGAACCTAGTTTGGGTGGGAATTAATACACTATTAT-----CAATATAGGAAAACTAAT 436  
| | | | |  
Db 213 AGCACCTTCTCTTACTTGGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272  
QY 437 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGATTTTATATATCTATATTCG 496  
| | | | |  
Db 273 AGGTAGTAGTGACAAATCCATATCAGATTGTCTATATGACTTATATATCTATATTGA 332  
QY 497 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTGTGATGCGATTGCGAGATTTTGCAGGTAAATTTGAA 556  
| | | | |  
Db 333 TTTCGCGGTAAAGTCAGAGTGTGTTTAAATGATGGGATGCGAGATTTTAAATGTTCTGTACT 392  
QY 557 AAATATAGAGAGTATTTATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 616  
| | | | |  
Db 393 CTTATACAGGAACTATTAGAGGCTCTGGATAGTGGAAATAGAAATCCTAATTTCTGCTTC 452  
QY 617 TCAAAAGACAAATTAATCTCGATATCGGACAAATAGTTTATTTTAAACTTTTCAGAAAG 676  
| | | | |  
Db 453 TCGTGAAGAACTCCGTAATGCGGCTGTTTAGAATGCGCGACTCAGAAATTTGATAGAAATTTAAC 512  
QY 677 AGATTTCAATGAAATTTCTAGGAGGGTCAATTTGTCAGAAACAAATGCTCAAGTATTTGTTATT 736  
| | | | |  
Db 513 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCAAATATTTATTTATT 572  
QY 737 ACTTACTTTTGCACAAAGCTGCAAAATGTGCAATTTATCTATTAAAGGATGCGAGTTCAATA 796  
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Db 573 ACCTTCTTTTGGAGCGCTGCAATTTTCCATTTATCTACTAAAGGATGCTACTAGATA 632  
QY 797 TAAAGCACAAATGTTCCCAATTTTNGATGCGAGAGATGTAAGATCGGAATTTATATCACC 856  
| | | | |  
Db 633 TGGCACTAATTTGGGGCTATACAATGCTACACCTTTATATAAATTTATCAATCAAACTAGT 692  
QY 857 TAAACAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTTAAATAATGCAAAACGGCAGA 916  
| | | | |  
Db 693 AGAGCTTATT-----GAACT 707  
QY 917 GTATACCAATTTATTTTATATTTGATATCGAGTAGGTTTAAATCAGATAAAACAGGGGG 976  
| | | | |  
Db 708 ATATACGTGATTTGCGTACATTTGGTATAATCGAGGTTTCAACGAACTAAGACAAACGAGG 767  
QY 977 GACAGTCTGACACTTGGTCCAAATTTAATAAATTTCTAGAGAAATGACGTTGCGGCT 1036  
| | | | |  
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTTTCATAGTATCGTAGAGAGATGACATTTGATGTT 837  
QY 1037 ATTGGATATTATCGCTATATTTTCCAACTTTATGATTTTGAGAAATATCCATTGCGCAACACA 1096  
| | | | |  
Db 828 ATTAGATATAGTAGCATCATTTTCAAGCTTGTATTTACTAATTAACCAATAGAAACAGA 887  
QY 1097 TGTAGAGTTGACTAGGAAATTTATACAGATCAGTGGGATTTATCATCGGAACTTTATAG 1156  
| | | | |  
Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATTTGGTTTGTGTACATCGTAGTGTCT 947  
QY 1157 TTGCTTACGGAATTCGCCTAATCTTTTAAATGGTTAGAGGCTAATGNAACACGGGACC 1216  
| | | | |  
Db 948 TAGGGGAGAAAGTTGGTTTGTGTTTAAATAGA-----GCTAATTTCTCAGATTTAGA 1001  
QY 1217 TGGTTTATGTTACTTGGCTTAGCAAAATAGGTATATATATATAGTATGTTTTCAGATATTT 1276  
| | | | |

|    |      |   |      |
|----|------|---|------|
| Db | 1002 | AAATGCAATACCTAATCCTAG-ACCGTCTTGGTGTTTTAAATAATATGATTTATCTACTG      | 1060 |
| Qy | 1277 | TGCGCGCTGGGTAGSAACTCGTCATTTATGAGACTACACAAAGGGTAAACGGTATTTTCA      | 1336 |
| Db | 1061 | GTTCACTTACATTTGCCGGTTAGCCCAAGTACTGATAGAGCGAGGGTATGG- - - - -TATGG | 1115 |
| Qy | 1337 | ACGTATGCTGGAACTACAGGTAATGATCTACGTAATATTTGATTTTCAGAAATGCCGATG      | 1396 |
| Db | 1116 | AAATCGAGATCGAAATTTCCCTGCTAAATTCACAAATTTATTTACTGAACTAATCTCTGGACA   | 1175 |
| Qy | 1397 | ATATAAAATTTACTTTCAATTTAGTATCATGAACCTTAGTAGGAGAGACTACCGCTAGACGAGA  | 1456 |
| Db | 1176 | ACATACGACTGCTACACAACTATTTTAGGGCGAAATATATTTAGAGTAGATTTCTCAAG- -    | 1234 |
| Qy | 1457 | GTAATCGTGTTCAAAGCGCAGATTTTCGTAGGGTAGGGGACCTGATTTTAAATTTATGATGC    | 1516 |
| Db | 1235 | - - -CTTGTAATTTAAATGATACCACATATGAGGTGAATAGGGCGGTATTTTATCATGATGC   | 1292 |
| Qy | 1517 | AGGTAATATGGGCTAAGCAGGATGACAAATGAACTCTACGTTCCCACTTGTAATGGCACTC     | 1576 |
| Db | 1293 | GAGTGAAGGTTCACAAAGATCCCGT- - - - -TACGAGGGGTATATTCGAA             | 1336 |
| Qy | 1577 | TAATGTGTTAGAGGACCTCTCATAGATTTACAAATGCGCATGTGTTGTATATGAAA          | 1636 |
| Db | 1337 | CAACTGGGATAGATAACCC- - - - -TAGAGTTCAAAATATTAACACTTATTTACCTGGAGA  | 1391 |
| Qy | 1637 | CTCCAGAGTTAACGTATATGTTGGACACATACAGTTTAAACGTAAGAAATATAATGGA        | 1696 |
| Db | 1392 | AAATTCAGATATCCCAACTCCAGAGACTATATCTCATATATTAAGCACACAATAAATTT       | 1451 |
| Qy | 1697 | AGCAATCAAAATTACACAAATACCGGGTGAAGAGTTATACCTTCAAAAATTTACTTGC        | 1756 |
| Db | 1452 | AACAGGAGGACTTTAGACAAAGTAGCATCTAATCCCGTTCATCTTTTAGTAATGATGTTG      | 1511 |
| Qy | 1757 | TAATGCTATACCTATGTAATAAAGCACTCAT- - -CAGGTGGGATTTAATCCGTTTT        | 1814 |
| Db | 1512 | GACACATAAAGTCTCGCTCGTAACAAATACCATTAATCCAGATAGAAATTACACAGATACC     | 1571 |
| Qy | 1815 | TTAAGAACAAAATCAGAGTATAACGAGTTTATGCAAGGTGGCGGAATTAGATTGATTT        | 1874 |
| Db | 1572 | TTTAGTGAAGGATTTAGAGTTTGGGGGGCACCTCTGTCAATACAGGACCAAGATTTAC        | 1631 |
| Qy | 1875 | AATAACAAAACCTCAGGACAAAGTTACCGTATTTTCGTTTATCGTGCAGATAAAGCT         | 1934 |
| Db | 1632 | AGGAGGGATATCCTTCGAAGAAATACCTTTGTGATTTTGTATCTCAAGTCAATAT           | 1691 |
| Qy | 1935 | GCCTTCTTTAGTGTATATCTTTATCCAGGAGGTGGGGTTCAAATCGTTTGTATCGCTT        | 1994 |
| Db | 1692 | TAATTCACCAAT-TACCCAAAGATACCGTTTAGATTTTCGTTACGCTTCCAGTAGGGATG      | 1750 |
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| Qy | 2175 | ACAACTTTTGAATATAGGGGAGAACGGGACCTTAGAAAAACAAAGAACCGGTGAACGAT       | 2234 |
| Db | 1916 | TAATTTGGGTAAGTGAACCACTCTATTTTGGTGCAGGTTCTATTTAGTAGCGGTGAACCTT     | 1975 |
| Qy | 2235 | CTGTTTTACCAATTAACAAATAATTTTACTAGATAGGGTGTATTCGCTTTTAA- - - - -CA  | 2291 |
| Db | 1976 | ATATAGATAAAATTTGAAATTTATTTCTAGCAGATGCAACATTTGAAAGCAGAAATCTGAT     | 2035 |
| Qy | 2292 | AATAAGCGAAAAAGTTGTGAGTCTCTATGTTTACAAAGTAGTAGCAAAAAATACGTTAAAA     | 2351 |
| Db | 2036 | AAAGAGCACAAAGGGGTGAATGCCCTGTGTTTACTTCTTCCCAATCAATCCGGGTAAAA       | 2095 |
| Qy | 2352 | THAGAAACGACAGATTTAGAAATAGATCAAGCGGCCATTTCTTATAGAAATGTATGTAGATG    | 2411 |
| Db | 2096 | CCGATGTGACGGATTTATCATATTTGATCAAGTATCCAAATTTAGTGATTTGTTTATCAGATG   | 2155 |
| Qy | 2412 | ACAAAAATCCTCAGAGAAAAATTAATGTTTATGGGATGAAATAAAACTGGCAAAACAACTTA    | 2471 |
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| Qy | 2472 | GTCACTCTCGTAATCTACTCCAAAATGGAGACTTTTCTGGGAATGATTTGGACATTCGGTA     | 2531 |
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| Qy | 2532 | ATGATATTATCATAGGATCCAAATAATCTTATTTTAAAGGAAAAATTTCTACAGATGCGTG     | 2591 |
| Db | 2276 | GTGGCTGGAGAGAAAGTACAGATATTACATCCAAAGGAGGAGATGACGTTATTCAAAGAGA     | 2335 |
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| Db | 2336 | ATTACGTCACTACCGGGTACCGTTGATGAGTGTCTTCAACGTTATTTATATCAGAAAA        | 2395 |
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| Qy | 2763 | TTCCAAATGATTTGGCCTTATATGACGCTTAATCTTTCATGTGGAGATTTACGCTGTGAT      | 2822 |
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QY 3123 AACACATGGAGAAAAACGTTGGGAAACACAAACAGCCTATGATCCAGCAAAACAGCGCTG 3182  
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| 23 | 120.8 | 5.8 | 2024  | 1 | BTU88188 | U88188 Bacillus th |
| 24 | 113.6 | 5.5 | 3931  | 1 | AB161456 | Bacillus th        |
| 25 | 106.6 | 5.1 | 3668  | 1 | AB185105 | AB185105 Bacillus  |
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ALIGNMENTS

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DEFINITION Sequence 13 from Patent WO2004074462.  
ACCESSION CQ868312  
VERSION CQ868312.1 GI:51998358  
KEYWORDS Bacillus thuringiensis  
SOURCE Bacillus thuringiensis  
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1  
AUTHORS Carozzi,N., Hargiss,T., Koziel,M.G., Duck,N.B. and Carr,B.  
TITLE Delta-endotoxin genes and methods for their use  
JOURNAL Patent: WO 2004074462-A 13 02-SEP-2004;  
Athenix Corporation (US)  
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ORIGIN

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| Qy  | 1921 | CAGATGGATGTGAGATGCAAGGGAATAGTTTCAATCAGATGTAACGCTGGTTCTCGAC | 1980 |  |
| Ds  | 2088 | CAGATGGATGTGAGATGCAAGGGAATAGTTTCAATCAGATGTAACGCTGGTTCTCGAC | 2147 |  |
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| Ds  | 2148 | AAATGGAATTCCTCCAGTAATACAACTTTTGAATATGAGGAGAACGGGACCTTA     | 2207 |  |
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| Bacillus thuringiensis  |      |  |      |  |
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| ORGANISM  |      |  |      |  |
| Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus     |      |  |      |  |
| cereus group.   |      |  |      |  |
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| Carozzi, N., Hargies, T., Koziel, M.G., Duck, N.B. and Carr, B.       |      |  |      |  |
| Delta-endotoxin genes and methods for their use                       |      |  |      |  |
| Patent: WO 2004074462-A 15 02-SEP-2004;                               |      |  |      |  |
| Athenix Corporation (US)  |      |  |      |  |
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| Qy | 190  | GGGATAAATCTTATAGAGTTTGTGATAGAACCCTAGTCTTGGGTGGAAATTAATACATTTTA   | 249  |  |
| Ds | 181  | GGGATAAATCTTATAGAGTTTGTGATAGAACCCTAGTCTTGGGTGGAAATTAATACATTTTA   | 240  |  |
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| Qy | 310  | GATTTATTATCTATTAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTATCGGATTGCA    | 369  |  |
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| Qy | 370  | GATTTTGACGGTAAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTATCGGATTGCA      | 429  |  |
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| Qy | 550  | AATGCTCAAGTATTTTCACTACTTTTGCACAAGCTGCAAAATGTGCAAGTATTACTTA       | 609  |  |
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| Ds | 961  | TATTCATCGGGAATTTATAGTTTGGTTACGGAATTCGCCCTTAATCTTTTAAATCGGTTAGAG  | 1020 |  |
| Qy | 1030 | GCTAATGGAACACGGGGACCTGTTTATGTTTACTTGGCTTAGCAAAATAGGTATATATAAT    | 1089 |  |
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## RESULT 4

AB074414  
LOCUS 3746 bp DNA linear BCT 14-JUN-2003  
DEFINITION Bacillus thuringiensis serovar aizawai cry40A and 4orf2 genes for putative mosquitocidal toxin and Cry400Rf2 protein, partial and complete cds.  
ACCESSION AB074414  
VERSION AB074414.1 GI:16945771  
KEYWORDS  
SOURCE Bacillus thuringiensis serovar aizawai

## ORGANISM

Bacillus thuringiensis serovar aizawai  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

## REFERENCE

AUTHORS

## TITLE

Cloning and Expression of Novel Crystal Protein Genes from Bacillus thuringiensis subsp. aizawai Encoding a Mosquitocidal Proteins

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 3746)

## AUTHORS

Ito, T., Sahara, K., Asano, S. and Bando, H.

## TITLE

Direct Submission

## JOURNAL

Submitted (14-NOV-2001) Takeshi Ito, Graduate school of Agriculture, Hokkaido University, Kita-9jyou Nishi-9chome, Kita-ku Sapporo-shi, Hokkaido 060-8589, Japan (E-mail: ito-toe@agr.hokudai.ac.jp, tel: 81-011-716-2487)

## FEATURES

## source

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Qy 1948 AGTTTTCAATCAGATGTAACGTTGTTCTCGACAAAATTTGAATTCCTCCCAAGTAATACA 2007

Db 2145 GACCTTGAAGTGGTGGAGCTCTTTATATCGACAAAATTTGAATTTATCCAGATGATTTA 2204

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Qy 2068 CTGTTTACCAATTA 2082

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RESULT 6

LOCUS Q0868325 2019 bp DNA linear PAT 13-SEP-2004

DEFINITION Sequence 26 from Patent WO2004074462.

ACCESSION Q0868325

VERSION Q0868325.1 GI:51998371

KEYWORDS Bacillus thuringiensis

SOURCE Bacillus thuringiensis

ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1

AUTHORS Carozzi, N., Hargies, T., Koziel, M. G., Duck, N. B. and Carr, B.

TITLE Delta-endotoxin genes and methods for their use

JOURNAL Patent: WO 2004074462-A 26 02-SEP-2004;

Athenix Corporation (US)

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 35.9%; Score 747.2; DB 6; Length 2019;

Best Local Similarity 69.8%; Pred. No. 8.1e-125;

Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

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Db 61 AATAACACAAATATGTCAAACAGATATCTTTTGCATAATTCGGATATGCTCTACTATG 120

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RESULT 7  
CQ868324  
LOCUS 2145 bp DNA linear PAT 13-SEP-2004  
DEFINITION Sequence 25 from Patent WO2004074462.  
ACCESSION CQ868324  
VERSION CQ868324.1 GI:51998370  
KEYWORDS Bacillus thuringiensis  
SOURCE Bacillus thuringiensis  
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1  
AUTHORS Carozzi,N., Hargies,T., Koziel,M.G., Duck,N.B. and Carr,B.  
TITLE Delta-endotoxin genes and methods for their use  
JOURNAL Patent: WO 2004074462-A 25 02-SEP-2004;  
Athenix Corporation (US)  
FEATURES  
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## ORIGIN

Query Match 35.9%; Score 747.2; DB 6; Length 2145;  
Best Local Similarity 69.8%; Pred. No. 8e-125;  
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

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Qy 181 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTAGTAGAACCTAGTTTGGGTGGAATTAAT 240  
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Db 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

RESULT 12
BD062618
LOCUS BD062618 3471 bp DNA linear PAT 27-AUG-2002
DEFINITION Toxins active against pests.
ACCESSION BD062618
VERSION BD062618.1 GI:22608221
KEYWORDS JP 2001507208-A/42.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 3471)
Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M. and Stockhoff, B.A.
Toxins active against pests
Patent: JP 2001507208-A 42 05-JUN-2001;
MYCOGEN CORP
FN JP 2001507208-A/42
PD 05-JUN-2001
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PF 01-JUL-1997 JP 1998504483  
PI ERNEST H SCHNEPF,CAROL WICKER,KENNETH E NARVA,MICHELE WALZ, PI  
BRIAN A STOCKHOF  
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CC Topology: Linear;  
FH Key Location/Qualifiers.

FEATURES  
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## ORIGIN

Query Match 8.1%; Score 168.6; DB 6; Length 3471;  
Best Local Similarity 52.5%; Pred. No. 1.3e-20;  
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

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Db 708 ATATAGTATTTAGTGGCTATCAATGTTGTTAATATCGAGGTTTCAACGAATTAAGAACAAGG 767  
Qy 810 GACAGGTGCTGACATTTGCTGAAATTTAATTAATTTTCTAGAGAAATGCAAGTTCGCGGT 869  
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTTTCAATAGATATCGTAGAGATGACATTTGATGTT 827  
Qy 870 ATTGGATATTTATCGCTATATTTTCCAACTTATGATTTTGAATAATCCATTTGCCACACA 929  
Db 828 ATTAGATATAGTAGCAATCAATTTTCAAGTCTTGTATTTACTAATTTACCCAATAGAAACAGA 887  
Qy 930 TGTAGAGTTCACTAGGAAATTTATACAGATCGAGTGGGATTTTCAATCGGGAATTTATAG 989  
Db 888 TTTTCAAGTTGAGTAGGCTATTTATACAGATCCAAATGTTGTTTGTATCATCGTAGTAGTCT 947  
Qy 990 TTTGGTTACGGAATTTGGCTTAATCTTTTAATGG 1022  
Db 948 TAGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

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| QY         | 990  | TTGGTTACGAATTCGCCCTAACTTTTAAATGG                              | 1022                                  |
| Db         | 948  | TAGGGAGAAAGTTGGTTAGCTTTTGAATAG                                | 980                                   |
| RESULT 13  |  |   |                                       |
| BD128371   |  |   |                                       |
| DEFINITION | 3471 bp  | DNA   | linear                                |
| ACCESSION  | BD128371   |   |                                       |
| VERSION    | BD128371.1   | GI:23223316   |                                       |
| KEYWORDS   | JP 2002500166-A/42.  |   |                                       |
| SOURCE     | unidentified   |   |                                       |
| ORGANISM   | unclassified.  |   |                                       |
| REFERENCE  | 1 (bases 1 to 3471)  |   |                                       |
| AUTHORS    | Schnepf, E.H., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and Cohn, J.M.                         |   |                                       |
| TITLE      | Toxin active on Ostrinianubilalis  |   |                                       |
| JOURNAL    | Patent: JP 2002500166-A 42 08-JAN-2002;  |   |                                       |
| COMMENT    | MYCOGEN CORP   |   |                                       |
|            | OS Unidentified  |   |                                       |
|            | PN JP 2002500166-A/42  |   |                                       |
|            | PD 08-JAN-2002   |   |                                       |
|            | PF 15-DEC-1998   |   |                                       |
|            | PI 31-DEC-1997   |   |                                       |
|            | PR ERNEST H SCHNEPF, CAROL WICKER, KENNETH E NARVA, MICHELE WALZ, PI BRIAN A STOCKHOFF, JUDY MULLER COHN |   |                                       |
|            | PC A01N63/02//C07K14/325,C12N15/09,C12N15/00   |   |                                       |
|            | CC Strandedness: Single;   |   |                                       |
|            | CC Topology: Linear;   |   |                                       |
|            | CC Toxin active on Ostrinianubilalis   |   |                                       |
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|            | Best Local Similarity  | 52.5%;  | Pred. No. 1.3e-20;                    |
|            | Matches  | 458; Conservative   | 0; Mismatches 364; Indels 51; Gaps 2; |
| QY         | 156  | AATTTGGGAATCAGTCGAACGATAACAAGTATTGGGATAAATCTTTATAGAGTTTCTGTAT | 215                                   |
| Db         | 153  | ANTAGCGGATGCGCAAAAGAACGAGTATCTATTGGGACACCAATAGTCTCTTTATCAC    | 212                                   |
| QY         | 216  | AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT   | 269                                   |
| Db         | 213  | AGCACCTCTCTTACTGGATTAAATTCATAGTATATGACCTTATAGGTAAAGTACTAGG    | 272                                   |
| QY         | 270  | TCGGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGTGATTTATCTATATAATTCG   | 329                                   |
| Db         | 273  | AGGTAGTAGTGGCAATCCATATCAGATTTGTCTATATGTGACTTATATCTATTATTGA    | 332                                   |
| QY         | 330  | TAAAGAGGTAGCGGATGTTTAAAGTGATGCGATTTCAGAGTTTTCAGCGTAAATTTGAA   | 389                                   |
| Db         | 333  | TTTACGGGTAGTCAGAGTGTTTAAATGATGGGATTGCAGATTTTAAATGGTTCTGTACT   | 392                                   |
| QY         | 390  | AAATTTAGAGATATTATCTTTCTTATCTTGGGGCTTGGCTTTAAAGACGGTAAACCACT   | 449                                   |
| Db         | 393  | CTTATACAGAACTATTAGAGGCTCTGGATAGCTGGAATAAGAACTCTAAATCTCTCTTC   | 452                                   |
| QY         | 450  | TCAAAGACAAATAATCTGATATCGGCAATTAGTTTATTTATTTTAAACCTTTCAGAAAG   | 509                                   |
| Db         | 453  | TGCTGAAGAACTCCGTACTCGTTTGTAGAAATCGCCGACTCAGAAATTTGATAGAAATTTA | 512                                   |
| QY         | 510  | AGATTTCAATGAATCTTAGGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTATT   | 569                                   |

|            |   |   |                                       |
|------------|---|---|---------------------------------------|
| Db         | 513   | CGAGGGTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAATATGCCAAATATTATTATT     | 572                                   |
| QY         | 570   | ACCTACTTTTGCACAAGCTGCAAATGTGCAGTTATTACTATTAAAGGATGCGATTCAATA    | 629                                   |
| Db         | 573   | ACCTTTCTTTTGGAGCGCTGCATTTTCCATTTTATTACTACTAAGGGATGCTACTAGATA    | 632                                   |
| QY         | 630   | TAAACACAATGGTTCCTCCATTTTTCAGTGCAGAGAAATGTAAAGATCGGAATTAATATCAC  | 689                                   |
| Db         | 633   | TGGCACTAAATTTGGGGGCTATACAAATGCTACACCTTTTATTAATTTATCAATCAAACTAGT | 692                                   |
| QY         | 690   | TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGCGAGA   | 749                                   |
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| Db         | 708   | ATATACTGATTATTCGGTACATTGCTATAATCGAGGTTTCAACGAATTAAGACAACGAGG    | 767                                   |
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| QY         | 990   | TGGTTTACGGAATTCGCCCTAATACTTTTAAATGG                             | 1022                                  |
| Db         | 948   | TAGGGGAGAAAGTTGGTTTAGCTTTGTTAATAG                               | 980                                   |
| RESULT 14  |   |   |                                       |
| AR205863   |   |   |                                       |
| LOCUS      | AR205863  | 3471 bp   | DNA                                   |
| DEFINITION | Sequence 71 from patent US 6369213.   |   | linear                                |
| ACCESSION  | AR205863  |   |                                       |
| VERSION    | AR205863.1  | GI:21503553   |                                       |
| KEYWORDS   | Unknown.  |   |                                       |
| SOURCE     | Unknown.  |   |                                       |
| ORGANISM   | Unclassified.   |   |                                       |
| REFERENCE  | 1 (bases 1 to 3471)   |   |                                       |
| AUTHORS    | Schnepf, H. Ernest., Wicker, C., Narva, K.E., Walz, M., Stockhoff, B.A. and Muller-Cohn, J. |   |                                       |
| TITLE      | Toxins active against pests   |   |                                       |
| JOURNAL    | Patent: US 6369213-A 71 09-APR-2002;  |   |                                       |
| FEATURES   | Location/Qualifiers   |   |                                       |
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|            | /mol_type='unassigned DNA'  |   |                                       |
| ORIGIN     |   |   |                                       |
|            | Query Match   | 8.1%;   | Score 168.6; DB 6; Length 3471;       |
|            | Best Local Similarity   | 52.5%;  | Pred. No. 1.3e-20;                    |
|            | Matches   | 458; Conservative   | 0; Mismatches 364; Indels 51; Gaps 2; |
| QY         | 156   | AATTTGGGAATCAGTCGAACGATAACAAGTATTGGGATAAATCTTTATAGAGTTTGTGAT    | 215                                   |
| Db         | 153   | AATAGCGGATGCGCAAAAGAACGAGTATCTATTGGGACACCAATAGTCTCTTTATCAC      | 212                                   |
| QY         | 216   | AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT     | 269                                   |
| Db         | 213   | AGCACCTCTCTTACTGGATTAAATTCATAGTATATGACCTTATAGGTAAAGTACTAGG      | 272                                   |
| QY         | 270   | TCGGACTAATCGTCAAACTGTGTCAGCACTTTCTATATGTGATTTATCTATATAATTCG     | 329                                   |
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Db 513 CCGAGGCTCTTAAACGAATGGTCTGTTAGCTAGACAAATGCCCAATATATTAAT 572
Qy 570 ACCTACTTTTGCACAGCTCGAATGTCAGATTTTACTTAAAGGATGCACTTCAATA 629
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Qy 690 TAAACAGTGGTGTGATTTTACCGGTGATTAATGAGCGAATTAATAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACCAATATGTTTATTTGTTATCAGGTAGGTTHAATCAGATATAAAGAGGGGG 809
Db 708 ATATACCTGATTTGCGTACATTTGGTATATCGAGGTTTCAACGAACTAAGACAACGAGG 767
Qy 810 GACAGGTGCTGACACTGGTGCAGAAATTTAATAAATTTGTPAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTACAGCTTGGTGTAGAAATTTATAGATATCGTAGAGATGACATTTGATGTT 827
Qy 870 ATTGGATATPATCGCTATATTTCCAACTATGATTTTGAGAAATATCCATTTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCTTTCAAGTCTTGATATTAATTTACCAATAGAAACAGA 887
Qy 930 TGTAGAGTTGACTAGGAAATTTATACAGATGAGTGGGATTTATTCATCGGAACTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAATTTGGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGGAAATGGCCTAATCTTTTAATGG 1022
Db 948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980
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RESULT 15
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DEFINITION Sequence 71 from patent US 6570005.
ACCESSION AR339971
VERSION AR339971.1 GI:33731211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3471)
AUTHORS Schnepf,H.E., Wicker,C., Narva,K.E., Walz,M. and Stockhoff,B.A.
TITLE Toxins active against pests
JOURNAL Patent: US 6570005-A 71 27-MAY-2003;
Mycogen Corporation; Indianapolis, IN
FEATURES
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Query Match 8.1%; Score 168.6; DB 6; Length 3471;  
Best Local Similarity 52.5%; Pred. No. 1.3e-20;  
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

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Qy 216 AGAACCTAGTTTGGGTGGAAATTAATACACTATTAT-----CAATTAATAGGAAACAAAT 269
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Qy 330 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTATGATGCGATTGTCAGATTTTGAACGTAATAAT 389
Db 333 TTTACGGGTAAAGTCAGAGTGTGTTTAAATGATGGGATTCAGATTTTAAAGTGTCTGTACT 392
Qy 390 AAATTATAGAGATATATCTTTCTTATCTTGGGCTTGGCTTTAAAGACGGTAAACCACT 449
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Qy 510 AGATTTCAATGAATTTCTAGGAGGTCATTTGTCAAGAAACAATGCTCAAGATTTGTTATT 569
Db 513 CCGAGGCTCTTTAAAGATGGTGGCTGTTAGCTAGACAAATGCCCAATATATTAATTT 572
Qy 570 ACTTACTTTTGCACAGCTGCAAAATGTGCAATTTTATCTTATTAAGGGATGCAAGTTCAATA 629
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Qy 630 TAAAGCACAATGGTTCCTCAATTTTGAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689
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Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACCAATATGTTTATTTGTTATCAGGTAGGTTTAAATCAGATATAAAGAGGGGG 809
Db 708 ATATACCTGATTTGCGTACATTTGGTATATCGAGGTTTCAACGAACTAAGACAACGAGG 767
Qy 810 GACAGGTGCTGACACTGGTGCAGAAATTTAATAAATTTGTPAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTACAGCTTGGTGTAGAAATTTATAGATATCGTAGAGATGACATTTGATGTT 827
Qy 870 ATTGGATATPATCGCTATATTTCCAACTATGATTTTGAGAAATATCCATTTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCTTTCAAGTCTTGATATTAATTTACCAATAGAAACAGA 887
Qy 930 TGTAGAGTTGACTAGGAAATTTATACAGATGAGTGGGATTTATTCATCGGAACTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAATTTGGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGGAAATGGCCTAATCTTTTAATGG 1022
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Job time : 6802.75 sec

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:03:30 ; Search time 5119.26 Seconds  
(without alignments)  
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Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaagatgagtcata.....acgatctgttaccataa 2082

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_est4:\*
- 5: gb\_est5:\*
- 6: gb\_est6:\*
- 7: gb\_est7:\*
- 8: gb\_est8:\*
- 9: gb\_est9:\*
- 10: gb\_est10:\*
- 11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| C 2        | 56    | 2.7         | 2087   | AG333887  | AG333887 Mus muscu  |
| C 3        | 54    | 2.6         | 1101   | CNS000D1  | AL065414 Drosophila |
| C 4        | 53    | 2.5         | 1101   | CNS000B7  | AL069440 Drosophila |
| C 5        | 52.8  | 2.5         | 874    | AZ533618  | AZ533618 ENTAC45TF  |
| C 6        | 52.2  | 2.5         | 1101   | CNS000EVL | AL069706 Drosophila |
| C 7        | 51.6  | 2.5         | 1101   | CNS0010X  | AL098379 Drosophila |
| C 8        | 51.2  | 2.5         | 1101   | CNS000EA9 | AL068837 Drosophila |
| C 9        | 50.6  | 2.4         | 548    | BI502178  | BI502178 kt86c11.y  |
| C 10       | 50.6  | 2.4         | 1101   | CNS017KX  | AL108171 Drosophila |
| C 11       | 50.2  | 2.4         | 486    | 2         | BG227627 kg11g12.y  |
| C 12       | 50.2  | 2.4         | 520    | 2         | BG227279 kg04g03.y  |
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| C 15       | 49.6  | 2.4         | 892    | 9         | AZ683446            |
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| C 17       | 49.4  | 2.4         | 1225   | 10        | CNS0161D            |
| C 18       | 49.2  | 2.4         | 1001   | 10        | CNS01400            |
| C 19       | 48.6  | 2.3         | 1101   | CNS000FVE | AL071298 Drosophila |
| C 20       | 48.4  | 2.3         | 928    | 10        | CNS000DKY           |
| C 21       | 48.4  | 2.3         | 1101   | 10        | CW942516            |
| C 22       | 48.2  | 2.3         | 1101   | 10        | CNS017ZQ            |

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|------|------|-----|------|----|-----------|
| C 23 | 48.2 | 2.3 | 1204 | 10 | CNS016E2  |
| C 24 | 47.8 | 2.3 | 893  | 10 | CNS013XE  |
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| C 26 | 47.8 | 2.3 | 996  | 9  | BH137139  |
| C 27 | 47.8 | 2.3 | 1101 | 10 | CNS016LI  |
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| C 31 | 47   | 2.3 | 1101 | 10 | CNS001FB  |
| C 32 | 47   | 2.3 | 1200 | 10 | CNS016CO  |
| C 33 | 46.8 | 2.2 | 1031 | 10 | CNS000CF2 |
| C 34 | 46.8 | 2.2 | 1035 | 10 | CNS002D5  |
| C 35 | 46.6 | 2.2 | 1101 | 10 | CNS0021J  |
| C 36 | 46.6 | 2.2 | 1101 | 10 | CNS00CYH  |
| C 37 | 46.4 | 2.2 | 1027 | 10 | CNS02T50  |
| C 38 | 46.4 | 2.2 | 1101 | 10 | CNS00Z62  |
| C 39 | 46.4 | 2.2 | 1225 | 10 | CNS0161D  |
| C 40 | 46   | 2.2 | 834  | 10 | CNS008CK  |
| C 41 | 46   | 2.2 | 1101 | 10 | CNS017KE  |
| C 42 | 45.8 | 2.2 | 612  | 9  | AZ523655  |
| C 43 | 45.8 | 2.2 | 863  | 9  | AZ692735  |
| C 44 | 45.6 | 2.2 | 886  | 9  | AZ672805  |
| C 45 | 45.6 | 2.2 | 963  | 10 | CNS00A4L  |

## ALIGNMENTS

RESULT 1  
CNS0039G/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

ORIGIN

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063921 GI:4941778

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mammoss in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers

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/organism="Drosophila melanogaster"

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/clone="BACR08K10"

/clone\_lib="RPCI-98"

/note="end : TET3"





[illegible]



COMMENT: Determination of this BAC-end sequence was carried out as part of a collaboration with the Human Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros' BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBel0BAC11.

DEFINITION

ACCESSION

VERSION

KEYWORDS

**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)

**REFERENCE** Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see http://www.fruitfly.org The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoshi Oseegawa and  
Aaron Mamoser at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw 9p, the same strain used for the BDGP's  
P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

**TITLE** Location/Qualifiers  
**JOURNAL** 1..1101  
**COMMENT** /organism="Drosophila melanogaster"  
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/db\_xref="taxon:7227"  
/clone="BACR28X21"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

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Best Local Similarity 41.6%; Pred. No. 0.46;  
Matches 187; Conservative 29; Mismatches 228; Indels 6; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 39  | TGAAATTTGGATCTTCATCGAATAACAATAAGCCCAACACAGATATCCTTTTGCNAA        | 98  |
| Db | 400 | TAAAAAANAAGTTTTATGATGAWAATWAAAATAAAAAAAAAAAWWAATTAAATTAATT       | 459 |
| Qy | 99  | TAATCGGGATATGTCTACTATGTCTTGGGAATGATGTGAGGAATCTCATGGGATGAAT       | 158 |
| Db | 460 | TAATTAATAATWAATATTAATAAANAATGATTTTGCGTTAAATAATATRAWTANGT         | 519 |
| Qy | 159 | TTGGGAATCGTGCAGAACATACAGATATGCGGATAATCTTATAGAGTTTGTGATAGA        | 218 |
| Db | 520 | ATATGAATTAATAAANAAGAAAGAAAGAAAGATTTAAAWAAAAATAAATATTAATA         | 579 |
| Qy | 219 | ACCTAGTTTGGGTGGAAATTAATACACTATTATCAATAATAGGAAACTAAATCCGACTAA     | 278 |
| Db | 580 | AATATGTTTAAGRTAATAAAGTAATAAANAATTAAGAAATATGAATTTGATTT-----A      | 633 |
| Qy | 279 | TGCTCAACATGTGTGACGACCTTCTATATGTGATTTATATCTATPAATTCGTAAGAGGT      | 338 |
| Db | 634 | ATGTATAAAGGGTTGAATTTATWAAGAAAAATTAATTTGAAAAATTAATAATTTTGAAGTTMAT | 693 |
| Qy | 339 | AGCCGATAGTGTTTTAAGTATGCGATTCGAGATTTTACGGTAATTTGAAAAATTTATAG      | 398 |
| Db | 694 | AAGAAAAAATTTAGAAAAAANAATTAAGAAATTAATAAAGATTTATTAATTTGAAATTAATG   | 753 |
| Qy | 399 | AGAGTATTATCTTTCTTATCTTGGGGCTTGGGCTTAAAGACGCTAAACCACTTTCAAAGAC    | 458 |
| Db | 754 | TTAGAAAAAATTTTTCGMAATGTTTATGMAATTTGMAATTTGMAATTTGMAATTTGMAATTT   | 813 |
| Qy | 459 | AAATAATTCGATATCGGACAATTAGTTTA                                    | 488 |
| Db | 814 | AAWAGATGTGTTATTTTWGAMAMTTTGTTKA                                  | 943 |

**ORIGIN**

**LOCUS** BI502178 548 bp mRNA linear EST 29-AUG-2001  
kt86c11.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter  
Strongyloides ratti cDNA 5' similar to TR:Q18989 Q18989 D2045.9  
PROTEIN [1] ; mRNA sequence.

**ACCESSION** BI502178.1 GI:15352567  
**VERSION** BI502178.1  
**KEYWORDS** Strongyloides ratti  
**SOURCE** Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Strongyloidea; Strongyloididae; Strongyloidea.  
1 (bases 1 to 548)

**REFERENCE** McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagaris, V., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Brandi Chiapelli and Dr. James  
McCarter (bchiapel@watson.wustl.edu & jmcarter@watson.wustl.edu) at  
Washington University, St. Louis. DNA Sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
High quality sequence stop: 395.

**FEATURES**  
Location/Qualifiers  
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/organism="Strongyloides ratti"  
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/dev\_stage="L2"  
/lab\_host="DH10B"  
/clone\_lib="Strongyloides ratti L2 pAMP1 v1 Chiapelli  
McCarter"  
/note="Vector: pAMP1 (Gibco); The library was constructed  
by Brandi Chiapelli and Dr. James McCarter at Washington  
University, St. Louis. The cDNA was made by using  
Dynabead oligo-dT priming (Dyna). PCR based library  
using a modified protocol from the SMART PCR cDNA  
Synthesis Kit from Clontech. Directionally cloned into the  
UDG sites of pAMP1. Nematodes were provided by Dr. Mark  
Viney of Bristol, UK."

**ORIGIN**

Query Match 2.4%; Score 50.6; DB 3; Length 548;  
Best Local Similarity 44.9%; Pred. No. 0.56;  
Matches 191; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 253 | ATAATAGGAAAACTAATTCGCACTAATCGTCAAACTGTGTCAGCACATTTCTATATGTGAT        | 312 |
| Db | 114 | ATATTAATAGAACCTATTATATAAATTTAAAAAATGGATTCTACTTAAACATTT               | 173 |
| Qy | 313 | TTATTATCTATAATTCGTAAGAGAGGTAGCCGATAGTGTTTTAAGTATGCGATTCGAGAT         | 372 |
| Db | 174 | GAAAAAGATAACATTTAGAAATGTTTGTATTAAGATTTCTAATGAATTTGAGGTATTCCTTCAT     | 233 |
| Qy | 373 | TTTGACGGTAAATTCGAAAAATTTATAGAGATATTATCTTTCTTATCTTGGGGCTTGGCTT        | 432 |
| Db | 234 | TCAGCTAAATTAATGAATATTCATTTATATCCATTTATCTTAATAATCAGTAATAATATGGAATTTTT | 293 |
| Qy | 433 | AAAGACGGTAAACCACTTTCAAAAGACAAATATTTCTGATATCGGCAATATGATTTATAT         | 492 |
| Db | 294 | TTTGACTATGAAATTTTAGAAAAAATCAGAAAGAGATTTAAATTAATTTATTTGTTGCT          | 353 |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 493 | TTTAAACTTTCAGAAAAGAGATTTCAATGAAATTCTAGAGGGTCATTGTCTCAAGAAAAAAT  | 552 |
| Db | 354 | AATAAGAATTTTCAGAAAGGTGATTTGTATCTTTACCATCATCTAAAAATTTTAAAAAAATCT | 413 |
| Qy | 553 | GCTCAAGTATGTATTACCTACTTTTGCCACAAGCTGCCAAATGTGCAGTTATTACTATTA    | 612 |
| Db | 414 | TACCCTAATTCCTCAATAGATTTCTTTTTTGATATAAAATTTATTAAATTTTAAAAAAGA    | 473 |
| Qy | 613 | AGGATCGAGTTCAATATAAGCACATGGTTCCTCATTTTTGAATGCGAGAAATGTGAAGA     | 672 |
| Db | 474 | AGTCAAAGAATCGAAAAAATCGATGAAATATTAAAAAACTGTGGTTTTTATGCTATGAAGA   | 533 |
| Qy | 673 | TCGGA   | 677 |
| Db | 534 | TGGA  | 538 |

|            |   |         |            |
|------------|---|---------|------------|
| RESULT 10  | CNS017KX/c  |         |            |
| LOCUS      | CNS017KX  | 1101 bp | DNA linear |
| DEFINITION | Drosophila melanogaster genome survey sequence S86 end of BAC HACN37F10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence. |         |            |

|           |   |            |  |
|-----------|---|------------|--|
| ACCESSION | AL108171.1  | GI:5628475 |  |
| VERSION   | AL108171.1  |            |  |
| KEYWORDS  | GSS.  |            |  |
| SOURCE    | Drosophila melanogaster (fruit fly)   |            |  |
| ORGANISM  | Drosophila melanogaster   |            |  |
|           | Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  |            |  |
| REFERENCE | 1 (bases 1 to 1101)   |            |  |
| AUTHORS   | Genoscope.  |            |  |
| TITLE     | Direct Submission   |            |  |
| JOURNAL   | Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  |            |  |
|           | - web : www.genoscope.cns.fr)   |            |  |
| COMMENT   | Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <a href="http://www.edgp.ebi.ac.uk">http://www.edgp.ebi.ac.uk</a> - This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector |            |  |

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FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:7227"
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            /plasmid="pBelobAC11"
            /note="end : SP6"
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|    | Query Match           | 2.4%  | Score 50.6;     | DB 10;     | Length 1101; |
|----|-----------------------|---|-----------------|------------|--------------|
|    | Best Local Similarity | 23.7%;  | Pred. No. 0.64; |            |              |
|    | Matches               | Conservative 181;   | Mismatches 210; | Indels 11; | Gaps 3;      |
| QY | 299                   | TTTCTATATGCGATTATATCTATATCGTAAAGAGGTAGCGGATAGTGTGTTTTAAGTC    | 358             |            |              |
| DB | 1101                  | TAKDDDWKDDTRTWTDKRRKKKTTWKTDKWRWTDTKDGGGGGGGKKKKGGSDRKAD      | 1042            |            |              |
| QY | 359                   | ATGCGGATTGCGAGATTTTGACGGTAAATTTGAAAAATATTAGAGAGTATTATCTCTTATC | 418             |            |              |
| DB | 1041                  | TKRDWRGAATRRARWATAATATADDTWKRTCTKRTWKWKWARRAAKWRDWDRTDW       | 982             |            |              |
| QY | 419                   | TTGGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAGACAAATAATCTTGATATCGGAC   | 478             |            |              |
| DB | 981                   | WDKWDTKWKDDRWTKGAWTGDGAGRAKRRDDERGDRGRRRRRRRTRKKKKWRRRAAWT    | 932             |            |              |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 479 | AATTAGTTTATTTATTTTAAACTTTTCAGAAAGAGATTTCATGAAATTTCTAGGAGGTGCAT  | 538 |
| Db | 921 | AWTTTMMGTTTGGAWTTKTRKGGGAAAAADWGTDDWRMDKRAAAAAGKDGKGKKART       | 862 |
| Qy | 539 | TGTCAGAAACAATTCGTCAAGTATTGTATTACTACT-----TTTGCACAAGCTGCAG       | 592 |
| Db | 861 | WGAAAAAAAWDDTKTATKTKKTKTGRAWAAAGRTTWDAAATAWTKRAAAAAGRRAAA       | 802 |
| Qy | 593 | ATGTGCAGTTATTACTATTAAAGGATCGAGTTTCAATATAAGACACAATGGTTCCTCAATTTT | 652 |
| Db | 801 | AWAKDRGTRKGRKRGRTDDGGKGTWKTKRTTWTAAARARRAAAAAGWT-----KTKT       | 746 |
| Qy | 653 | TGAGTCAGAGAAATGTAAAGATCGGAATTAATATCACCTAACAGTCGTGTGTGATTTTACCG  | 712 |
| Db | 745 | DGRRARAADAWTTTTRKGAATRDRAAAAAAATTRCGAAAAAATGGKTTDAGAAAAATAWA    | 686 |
| Qy | 713 | GTGATTACTATGAG-CGATTTAAATCGAAACGGCAGAGTATACCAATTTATTTGTTTATAT   | 771 |
| Db | 685 | WRTTWTWDWAAARAAGAAWAAJAAADWDAADKKKGRRARKRAAATAARRAKKAKKD        | 636 |
| Qy | 772 | TGTTATCAGTAGGTTTTAAATCAGATAAAACAGGGGGGACAGGTGC                  | 818 |
| Db | 625 | RRGGGGGGSSSGGSCSSVCCVCVSAVAMAGGGGGGRRRVGAGGS                    | 579 |

|            |  |             |   |
|------------|--|-------------|---|
| RESULT 11  | 486 bp   | linear      | EST 09-MAY-2001                         |
| BG227627   | kg11g12.v1   | TBN95TW-SSR | Strongyloides stercoralis cDNA 5', mRNA |
| LOCUS      | sequence.  |             |   |
| DEFINITION | BG227627   |             |   |
| ACCESSION  | BG227627.1   | GI:12715182 |   |
| VERSION    | EST.   |             |   |
| KEYWORDS   | Strongyloides stercoralis  |             |   |
| SOURCE     | Strongyloides stercoralis  |             |   |
| ORGANISM   | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloidea; Strongyloides.   |             |   |
| REFERENCE  | 1 (bases 1 to 486)   |             |   |
| AUTHORS    | McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M., Hillier, L., Kubacka, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. |             |   |
| TITLE      | The Washington Univ. Nematode EST Project, 1999  |             |   |
| JOURNAL    | Unpublished (1999)   |             |   |

**TITLE**  
The Washington Univ. Nematode EST Project, 1999  
**JOURNAL**  
Unpublished (1999)  
**COMMENT**  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Dr. Thomas Nutman and colleagues of  
NIAD, NIH (tnutman@nih.gov). DNA sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
High quality sequence stop: 411.

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FEATURES
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                /organism="Strongyloides stercoralis"
                /mol_type="mRNA"
                /strain="Rhabbitiform larvae obtained from gerbils"
                /db_xref="taxon:6248"
                /lab_host="XL-1 Blue MRF" (Stratagene)
                /clone_lib="TBN95TM-SSR"
                /note="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1:
                    EcoRI; Site 2: XhoI; mRNA was purified from 2 x 103
                    Rhabbitiform larvae which had been isolated from gerbils
                    experimentally infected with larvae originally isolated
                    from experimentally infected dogs. cDNA was constructed
                    and, using adaptors, was cloned unidirectionally into the
                    vector from the EcoRI site to the XhoI site. The library

```

has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."

ORIGIN

Query Match 2.4%; Score 50.2; DB 2; Length 486;  
Best Local Similarity 50.6%; Pred. No. 0.69;  
Matches 121; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 344 ATAGTGTGTTTAAGTCGATCGGATTCGACGATTTTGACGGTAAATTTGAAAAATTTATAGAGCT 403  
DB 105 AGATTGATTCATAGAAAATGAATTAGAAGTGGTGGTATTATATAAAAATTTTAGAATA 164  
QY 404 ATTATCTTTCTTATCTTGGGCTTGCTTTAAAGACGGTAAACCCACTTCAAAAGACAAATA 463  
DB 165 TAGACAAGTCAAGTAATAGTAATTCAGATTCAGATGTGAACAACAATAATACAAATG 224  
QY 464 ATTCTGATTCGCAACAATTAGTTTATTTTAACTTTTCAGAAAGAGATTTCAATGAAA 523  
DB 225 AGACATTTCAAGGATCTCTCAGGAAATTCACACCTTGACATTTGATGATGATTTAAAAA 284  
QY 524 TTCTAGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTTATACCTACTTTTGCA 582  
DB 285 TTCAAAGCGGGTCATTTTAAAGTAAGAATAATACAGATTTATTAGAAACAAGTATTGAA 343

RESULT 12  
BG227279  
LOCUS  
DEFINITION  
Qk04903.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5', mRNA  
sequence.  
BG227279  
BG227279.1 GI:12714834  
EST.  
Strongyloides stercoralis  
Strongyloides stercoralis  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Panagrolaimidae; Strongyloidea; Strongyloides.

REFERENCE  
1 (bases 1 to 520)  
Wyllie, T., Dente, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu  
The library was constructed by Dr. Thomas Nutman and colleagues of  
NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
High quality sequence stop: 405.

Location/Qualifiers  
1. .520  
/organism="Strongyloides stercoralis"  
/mol\_type="mRNA"  
/strain="Rhabditiform larvae obtained from gerbils"  
/db\_xref="taxon:6248"  
/lab\_host="XL-1 Blue MRF" (Stratagene)"  
/clone\_lib="TBN95TM-SSR"  
/notes="Vector: Lambda Uni-ZAP XR (Stratagene); Site 1:  
EcORI; Site 2: XhoI; mRNA was purified from 2 x 10E3  
rhabditiform larvae which had been isolated from gerbils  
experimentally infected with larvae originally isolated  
from experimentally infected dogs. cDNA was constructed

and, using adaptors, was cloned unidirectionally into the  
vector from the EcoRI site to the XhoI site. The library  
has an unamplified titer of 1 x 10E5 pfu/ml and an  
amplified, undiluted titer of 9 x 10E11 pfu/ml. The  
average insert size of the unamplified library is 675 bp  
(range, 100-1700)."

ORIGIN

Query Match 2.4%; Score 50.2; DB 2; Length 520;  
Best Local Similarity 50.6%; Pred. No. 0.7;  
Matches 121; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 344 ATAGTGTGTTTAAGTCGATCGGATTCGACGATTTTGACGGTAAATTTGAAAAATTTATAGAGCT 403  
DB 105 AGATTGATTCATAGAAAATGAATTAGAAGTGGTGGTATTATATAAAAATTTTAGAATA 164  
QY 404 ATTATCTTTCTTATCTTGGGCTTGCTTTAAAGACGGTAAACCCACTTCAAAAGACAAATA 463  
DB 165 TAGACAAGTCAAGTAATAGTAATTCAGATTCAGATGTGAACAACAATAATACAAATG 224  
QY 464 ATTCTGATTCGCAACAATTAGTTTATTTTAACTTTTCAGAAAGAGATTTCAATGAAA 523  
DB 225 AGACATTTCAAGGATCTCTCAGGAAATTCACACCTTGACATTTGATGATGATTTAAAAA 284  
QY 524 TTCTAGAGGGTCATTGTCAAGAAACAATGCTCAAGTATTGTTTATACCTACTTTTGCA 582  
DB 285 TTCAAAGCGGGTCATTTTAAAGTAAGAATAATACAGATTTATTAGAAACAAGTATTGAA 343

RESULT 13  
CNS006N9  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence T7 end of BAC #  
BACR14J19 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL065781.1 GI:4944661  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 964)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mammos in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers  
1. 964  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR14J19"  
/clone\_lib="RPCI-98"  
/note="end : T7"

ORIGIN



Query Match 2.4%; Score 50; DB 10; Length 964;  
 Best Local Similarity 30.9%; Pred. No. 0.87; Mismatches 195; Indels 3; Gaps 2;  
 Matches 137; Conservative 108

QY 4 AAAAGATGAGTCCATATCAAAATATAAATGAATATGAATATGGAATCCTCATCGAAT 63  
 DB 521 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 580  
 QY 64 AACACAAATACGCCAACAGATATCTTTTGGCAATATCGGATATGTCATATGTCT 123  
 DB 581 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 640  
 QY 124 TCGAATGATGTCAGGGAATCTCATGGATGAAT--TTGGGAATCAGTCGAACGATAA 181  
 DB 641 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 700  
 QY 182 CAAGTATGCGGATAAATCTTATAGAGTTGTGTAGAACCTAGTTTGGGTGGGAATTAATA 241  
 DB 701 ADAADAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 760  
 QY 242 CACTATATCAATAATAGGAACTAATTCGGAATATCGTCAACCTGTGTGAGCACTTT 301  
 DB 761 AADTAKAKWDADKDDKAGAKADKARKAANAANAANAANAANAANAANAANAANAANA 820  
 QY 302 CTATATGATGTTATATCTATATATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATG 361  
 DB 821 AGTGAAKARAGKA--TAGAGAGAKAKAKDKKAGDKADAKADAKADAKADAKADAK 879  
 QY 362 CGATTCAGATTTTGGCGTAAATTCGAAATATATAGAGATATATCTTCTTATCTTG 421  
 DB 880 AGADKAGAKAKKGGKANAGDAKAKAKAANAANAANAANAANAANAANAANAANAANA 939  
 QY 422 GGGCTTGGCTTAAAGACGGTAAA 444  
 DB 940 KDAADKAKAKKADAKKAKGWAKA 962

RESULT 14  
 BH152435/c  
 LOCUS  
 DEFINITION  
 ENT0G777R Entamoeba histolytica Sheared DNA linear GSS 28-AUG-2001  
 genomic, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Entamoeba histolytica  
 Entamoeba histolytica  
 Eukaryota; Entamoebidae; Entamoeba.  
 1 (bases 1 to 923)  
 Lofus, B., Wang, Z., Van Aken, S. and Fraser, C.  
 Determination of clone end sequences from Entamoeba histolytica  
 HMI:IMSS sheared DNA library (2001)  
 Unpublished (2001)  
 Contact: Brendan J Loftus  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0208  
 Fax: 301 838 3543  
 Email: bjlloftus@tigr.org  
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared  
 DNA library  
 Seq primer: M13-Reverse  
 Class: shotgun  
 High quality sequence start: 18  
 High quality sequence stop: 658.  
 Location/Qualifiers  
 1..923  
 /organism="Entamoeba histolytica"  
 /mol\_type="genomic DNA"  
 /strain="HMI:IMSS"  
 /db\_xref="taxon:5759"

FEATURES  
 source

/clone lib="Entamoeba histolytica Sheared DNA"  
 /note="Vector: pHS1; Site 1: Bst I; Constructed at The  
 Institute for Genomic Research (TIGR), Rockville, MD.  
 Genomic DNA isolated from broth cultures of E. histolytica  
 using a method described by Clark and Diamond (Clark,  
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a  
 method for isolate identification. Exp. Parasitol.  
 77:450.). The DNA was mechanically sheared to give a  
 tight size distribution (~2 kb). The v + i method used for  
 the library construction is described in detail in Smith,  
 H.O. and Venter, J.C. (Making small insert libraries for  
 whole genome shotgun sequencing projects. In Genome  
 Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Borell, Oxford University Press, 1999)."

## ORIGIN

Query Match 2.4%; Score 49.8; DB 9; Length 923;  
 Best Local Similarity 45.7%; Pred. No. 0.96;  
 Matches 174; Conservative 0; Mismatches 207; Indels 0; Gaps 0;

QY 246 ATTATCAATAATAGGAACTAATTCGGAATATCGTCAACCTGTGTGAGCACTTTCTAT 305  
 DB 383 ATAATAAATAAATTCGGAATCTTTTACACATATCTTGAACAGATAATAAATAAATAT 324  
 QY 306 ATGTGATTTTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAAGTGATCGAT 365  
 DB 323 TATTTATTTAATAGTTATATTTTCATCATATTTGAGAAGTGAATGTTTCACTTTATTCGTC 264  
 QY 366 TCGAGATTTTGAAGTAAATTCGAAATATATAGAGATATATCTTTCTTCTTCTTGGGGC 425  
 DB 263 ATGATTTTATTTCTTGTGAATCATGCTTTTCAACCATCATTAATAATAAATATTTCTCAT 204  
 QY 426 TTGGCTTAAAGAGCGGTAAACCACTTCAAAAGACAATAATTCGTATATCGGACAATAGT 485  
 DB 203 TAAAGTTGTTATTTAGTTTGAATTTAATGATTTATTAATACTCACCATTCTTTATTTAT 144  
 QY 486 TTATTATTTTAAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTGATTTGCAAG 545  
 DB 143 ATTTATGTTGAATATATCTAATAACAGTTGATTTGATTTGATTTGATTTGATTTGATTT 84  
 QY 546 AAACAATGCTCAAGTATTTGTTTATTTACCTACTTTTGCACAAGCTGCAAAATGTCAGTTAT 605  
 DB 83 ATTCATTATCACTTTGCTTAAATAATACCAGTACATTCAATTCATAATTAATTAATA 24  
 QY 606 ACTATTAGCGATGCGATTCA 626  
 DB 23 AATATACATGCTTCCAGCACA 3

RESULT 15  
 AZ683446/c  
 LOCUS  
 DEFINITION  
 ENTIR777R Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000  
 genomic, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Entamoeba histolytica  
 Entamoeba histolytica  
 Eukaryota; Entamoebidae; Entamoeba.  
 1 (bases 1 to 892)  
 Lofus, B., Van Aken, S. and Fraser, C.  
 Determination of clone end sequences from Entamoeba histolytica  
 HMI:IMSS sheared DNA library  
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 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared  
 DNA library  
 Seq primer: M13-Reverse  
 Class: shotgun  
 High quality sequence start: 18  
 High quality sequence stop: 658.  
 Location/Qualifiers  
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 /strain="HMI:IMSS"  
 /db\_xref="taxon:5759"

FEATURES  
 source

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Lofus, B., Van Aken, S. and Fraser, C.  
 Determination of clone end sequences from Entamoeba histolytica  
 HMI:IMSS sheared DNA library  
 Unpublished (2000)  
 Contact: Brendan J Loftus  
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 Fax: 301 838 3543  
 Email: bjlloftus@tigr.org  
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 09:48:39 ; Search time 770.097 Seconds  
(without alignments)  
18018.361 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaaagatggtccata.....acgatctgttaccacattaa 2082

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID          | Description        |
|------------|-------|---------------|--------|-------------|--------------------|
| 1          | 2082  | 100.0         | 2082   | 13 ADR89401 | Adt-89401 AXMI-008 |
| 2          | 2082  | 100.0         | 5980   | 13 ADR89400 | Adt-89400 AXMI-008 |
| 3          | 2073  | 99.6          | 2073   | 13 ADR89403 | Adt-89403 AXMI-008 |
| 4          | 747.2 | 35.9          | 2019   | 13 ADR89414 | Adt-89414 AXMI-008 |
| 5          | 747.2 | 35.9          | 2145   | 13 ADR89413 | Adt-89413 AXMI-008 |
| 6          | 739.8 | 35.5          | 2010   | 13 ADR89416 | Adt-89416 AXMI-008 |
| 7          | 170.2 | 8.2           | 1983   | 3 AAZ93234  | Aaz93234 Sequence  |
| 8          | 170.2 | 8.2           | 3837   | 3 AAZ93235  | Aaz93235 Sequence  |
| 9          | 168.6 | 8.1           | 3471   | 2 AAX83876  | Aax83876 Bacillus  |
| 10         | 168.6 | 8.1           | 3471   | 2 AAX83876  | Aax83876 Bacillus  |
| 11         | 160.6 | 7.7           | 2407   | 4 AAS02478  | Aas02478 B. thurin |
| 12         | 102.4 | 4.9           | 4366   | 8 ABX13497  | Abx13497 B. popill |
| 13         | 102.4 | 4.9           | 4366   | 14 AEB90830 | Aeb90830 Paenibaci |
| 14         | 99.6  | 4.8           | 1986   | 13 ADR89411 | Adt-89411 AXMI-009 |
| 15         | 99.6  | 4.8           | 2016   | 13 ADR89409 | Adt-89409 AXMI-009 |
| 16         | 99.6  | 4.8           | 2049   | 13 ADR89407 | Adt-89407 AXMI-009 |
| 17         | 95.6  | 4.6           | 3687   | 4 AAH28240  | Aah28240 Nucleotid |
| 18         | 95.6  | 4.6           | 4173   | 4 AAS02482  | Aas02482 B. thurin |
| 19         | 95.2  | 4.6           | 4359   | 8 ABX13486  | Abx13486 B. popill |

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|----|------|-----|------|-------------|--------------------|
| 20 | 95.2 | 4.6 | 4359 | 14 AEB90814 | Aeb90814 Paenibaci |
| 21 | 94.4 | 4.5 | 1959 | 4 AAS02466  | Aas02466 B. thurin |
| 22 | 93.4 | 4.5 | 3684 | 2 AAV15222  | Aav15222 Bacillus  |
| 23 | 93.4 | 4.5 | 3684 | 4 AAB99221  | Aab99221 Bacillus  |
| 24 | 93.4 | 4.5 | 3684 | 4 AAS02489  | Aas02489 B. thurin |
| 25 | 93   | 4.5 | 1897 | 3 AAZ39905  | Aaz39905 Truncated |
| 26 | 93   | 4.5 | 1897 | 4 AAH26983  | Aah26983 Coding se |
| 27 | 93   | 4.5 | 2019 | 8 ABV93758  | Abv93758 B. thurin |
| 28 | 93   | 4.5 | 2019 | 8 ABV93759  | Abv93759 B. thurin |
| 29 | 93   | 4.5 | 2019 | 8 ABV93756  | Abv93756 Bacillus  |
| 30 | 93   | 4.5 | 2019 | 8 ABV93757  | Abv93757 B. thurin |
| 31 | 93   | 4.5 | 3471 | 2 AAV16516  | Aav16516 DNA encod |
| 32 | 93   | 4.5 | 3471 | 2 AAX83877  | Aax83877 Bacillus  |
| 33 | 93   | 4.5 | 3471 | 4 AAS02477  | Aas02477 B. thurin |
| 34 | 93   | 4.5 | 3474 | 4 AAH19323  | Aah19323 Cry9C cod |
| 35 | 93   | 4.5 | 4344 | 2 AAQ56782  | Aaq56782 Insectici |
| 36 | 93   | 4.5 | 4344 | 2 AAV99986  | Aav99986 Nucleotid |
| 37 | 92.8 | 4.5 | 1897 | 2 AAV13118  | Aav13118 Bacillus  |
| 38 | 92.8 | 4.5 | 3687 | 12 ADK98478 | Adk98478 B thuring |
| 39 | 92.8 | 4.5 | 3932 | 2 AAQ64112  | Aaq64112 cryET5 ge |
| 40 | 92.8 | 4.5 | 3932 | 2 AAZ09160  | Aaz09160 B. thurin |
| 41 | 92.8 | 4.5 | 3934 | 2 AAT95051  | Aat95051 DNA encod |
| 42 | 92.8 | 4.5 | 3934 | 2 AAT68434  | Aat68434 CryET5 ge |
| 43 | 92.8 | 4.5 | 3934 | 2 AAV83927  | Aav83927 DNA encod |
| 44 | 92.8 | 4.5 | 6930 | 6 AAD43973  | Aad43973 Bacillus  |
| 45 | 92.8 | 4.5 | 6930 | 10 ADF31299 | Adf31299 Bacillus  |

## ALIGNMENTS

RESULT 1

ADR89401

ID ADR89401 standard; cDNA; 2082 BP.

XX

AC ADR89401;

XX

DT 18-NOV-2004 (first entry)

XX

DE AXMI-008 coding sequence.

XX

ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
expression cassette; transformation; transgenic; plant; bacteria;  
lepidoptera; coleoptera; pest; pesticide; resistance;  
pesticidal activity.

OS Bacillus thuringiensis.

XX

FH Key Location/Qualifiers

CDS 1..2082

FT /\*tag= a

FT /product= "AXMI-008"

FT /transl\_except= pos:1..3, aa:Met

XX WO2004074662-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782096.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

|    |   |  |
|----|---|--|
| PA | (ATHE-) ATHENIX CORP.   |  |
| XX | Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;                         |  |
| XX | WPI: 2004-635574/61.  |  |
| DR | P-PSDB; ADR89402.   |  |
| XX | New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids |  |
| PT | and polypeptides, useful for killing lepidopteran or coleopteran pests or |  |
| PT | for producing organisms with pesticide resistance.                        |  |
| XX | Claim 1; SEQ ID NO 13; 178pp; English.                                    |  |
| XX | This sequence encodes an isolated delta-endotoxin. Some of the delta-     |  |
| CC | endotoxin coding sequences of the invention have alternative start        |  |
| CC | codons, producing more than one protein from a single open reading frame. |  |
| CC | The nucleic acid sequences of the invention are useful in DNA constructs  |  |
| CC | or expression cassettes for transformation and expression in plants and   |  |
| CC | bacteria. The nucleic acids and corresponding polypeptides are useful for |  |
| CC | killing lepidopteran or coleopteran pests. Compositions containing the    |  |
| CC | delta-endotoxins of the invention, and methods for their production, are  |  |
| CC | useful for the production of organisms with pesticide resistance,         |  |
| CC | specifically bacteria and plants. These organisms are useful for          |  |
| CC | generating altered or improved delta-endotoxin or delta-endotoxin-        |  |
| CC | associated proteins that have pesticidal activity, or for detecting the   |  |
| CC | presence of delta-endotoxin or delta-endotoxin-associated proteins or     |  |
| CC | nucleic acids in products or organisms.                                   |  |
| XX | Sequence 2082 BP; 699 A; 305 C; 434 G; 644 T; 0 U; 0 Other;               |  |
| SQ | Query Match 100.0%; Score 2082; DB 13; Length 2082;                       |  |
|    | Best Local Similarity 100.0%; Pred. No. 0;                                |  |
|    | Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;             |  |
| QY | 1 GTGAAAAGATGAGTCCATATCAAAATATAAAATGAATATGAATATTTGGAATCCTCATCG 60         |  |
| DB |   |  |
| QY | 61 AATAACACAATAACGCCAAACAGATATCCTTTTGCAAAATAATCGGATATGCTACTATG 120        |  |
| DB |   |  |
| QY | 121 TCTTGGAAATGATGTGAGGGAATCTCATGCGGATGAAATTTGGGAATCAGTCGAAACGATA 180     |  |
| DB |   |  |
| QY | 181 ACAAGTATTCGGGATAAATCTTATAGAGTTTGTGATAGAACTAGTTTGGGTGGAATTAAT 240      |  |
| DB |   |  |
| QY | 241 ACATATTAATCAATAATAGGAAACTAAATCCGACTAATCGTCAAACTGTGTGAGCACTT 300       |  |
| DB |   |  |
| QY | 301 TCTATATGATTTATATCTATAATTCGTAAGAGTAGCCGATAGTGTGTTAAAGTAT 360           |  |
| DB |   |  |
| QY | 361 GCGATTGCGAGTTTTCGCGGTAAATTCGAAATTTATAGAGAGTATTATCTTCTTATCTT 420       |  |
| DB |   |  |
| QY | 421 GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTGATATCGGACAA 480       |  |
| DB |   |  |
| QY | 481 TTAGTTTATTTTAAACTTTCAGAAAGAGATTTCAATGAAATTTCTAGAGGGTCATTG 540         |  |
| DB |   |  |
| QY | 541 TCAGAAACAAATGCTCAAGTATTTGTTATTAACCTTTTTCACAAAGCTGCAAAATGTGCAG 600     |  |
| DB |   |  |
| QY | 601 TTATTAATTAAGGATGCAAGTTCATATATAAAGCAATGGTCCCAATTTTGGATGCA 660          |  |
| DB |   |  |
| QY | 661 GAGATGTAAGATCGGAATTAATCACTAACAGTGGTCTGATTTTACCGGTGATTAC 720           |  |
| DB |   |  |
| QY | 721 TATGAGCGATTTAAATGCAAAACCGCAGATATACCAATTAATTTGTTATATGGTATCAG 780       |  |
| DB |   |  |
| QY | 781 GTAGTTTAAATCAGATATAAACAAGGGGGGACAGTGTCTGACACTTGGTCCAAATTTAAT 840      |  |
| DB |   |  |
| QY | 841 AAATTTCTAGAGAAATGACGTTGCGGTATTTGGATATTTATCGCTATATTTCCAACTTAT 900      |  |
| DB |   |  |
| QY | 901 GATTTTGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT 960     |  |
| DB |   |  |
| QY | 961 GCAGTGGGATATTCATTCGGGAACTTATATAGTTGGTTACGGAATTTGGCCCTAACTTTTAAAT 1020 |  |
| DB |   |  |
| QY | 1021 GGGTTAGAGGCTTAAGGAACACGGGGACCTGGTTTAGTTTACTTGGCTTAGCAAAATAGT 1080    |  |
| DB |   |  |
| QY | 1081 ATATATAATGAGTATGTTTCGAGATATTTTCCGGCTGGGTAGGAACCTCGTCATTATGAA 1140    |  |
| DB |   |  |
| QY | 1141 GACTACAACAAGGGTAAACGGTATTTTCAAGCTATGTCGGAACTACGAGTAAATGATCTA 1200    |  |
| DB |   |  |
| QY | 1201 CGTATATTTGATTTTTCAGAACTCCGATGATATAAAATTTACTTCATTAGCTATCATGAAC 1260   |  |
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| QY | 1261 CTAGTAGGAGAGACTACCGCTAGACAGATATCGTGTTCAAAGGCGAGATTTTCGTAGG 1320      |  |
| DB |   |  |
| QY | 1321 GTAGGGGACCTGATTTAAATTAATGATGAGGTAATAATGGGCTAAGCAGGATGACAAAT 1380     |  |
| DB |   |  |
| QY | 1381 GAACTCTAGTTCCTGATTTGATTTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440     |  |
| DB |   |  |
| QY | 1441 TCAAAATCGGCACTGTGTTGTATATATGGAACCTCCAGAGTTAACTGATATGGTTGGACAT 1500   |  |
| DB |   |  |
| QY | 1501 ACAAGTTTAAACCGTGAATAATAATTAAGAGCAATCAAAATACAAATACCGGGGTG 1560        |  |
| DB |   |  |
| QY | 1561 AAGAGTTTAAACCGTGAATAATAATTAAGAGCAATCAAAATACAAATACCGGGGTG 1620        |  |
| DB |   |  |
| QY | 1621 CATACAGGTGGGATTTAATCCGTTTAAAGAACAAAATCAGAGTATAACCGAGTTTAT 1680       |  |
| DB |   |  |

|    |      |  |      |
|----|------|--|------|
| Qy | 1581 | GCAGGTGGCGGAATTAGATTGAATTATTAAATACAAAACCTGCAGACAAAAGTTACCGTATT   | 1740 |
| Db | 1581 | GCAGGTGGCGGAATTAGATTGAATTATTAAATACAAAACCTGCAGACAAAAGTTACCGTATT   | 1740 |
| Qy | 1741 | CGTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTTAGTGATATCTTTTATCCAGGAGGT   | 1800 |
| Db | 1741 | CGTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTTAGTGATATCTTTTATCCAGGAGGT   | 1800 |
| Qy | 1801 | TGGGGTTCAAATCGTTTTTGTATCGCTTGA AAAAATCTTACTCTGGAAATTTATGACGATTTA | 1860 |
| Db | 1801 | TGGGGTTCAAATCGTTTTTGTATCGCTTGA AAAAATCTTACTCTGGAAATTTATGACGATTTA | 1860 |
| Qy | 1861 | AAATATAGTGAATTTTAAATTCGCTGGAATTTATCACACTCGATACCTAGTTCAAACATT     | 1920 |
| Db | 1861 | AAATATAGTGAATTTTAAATTCGCTGGAATTTATCACACTCGATACCTAGTTCAAACATT     | 1920 |
| Qy | 1921 | CAGATGAGTGTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGTGGTTCTCGAC    | 1980 |
| Db | 1921 | CAGATGAGTGTGGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAACGTGGTTCTCGAC    | 1980 |
| Qy | 1981 | AAAATTGAAATTCCTCCCAAGTAAATACAAACATTTTGAATATAGGCGAGAACCGGACCTA    | 2040 |
| Db | 1981 | AAAATTGAAATTCCTCCCAAGTAAATACAAACATTTTGAATATAGGCGAGAACCGGACCTA    | 2040 |
| Qy | 2041 | GA AAAAACAAGAAACGGGTGAACGATCTGTGTTACCAATTAA                      | 2082 |
| Db | 2041 | GA AAAAACAAGAAACGGGTGAACGATCTGTGTTACCAATTAA                      | 2082 |

## RESULT 2

ADR89400

ADR89400  
ID ADR89400 standard; cDNA: 5980 BP.

XX  
XX  
OFFENSES

AC ADR89400:

AC  
ADK03400;  
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18-NOV-2004 (First entry)

DT 18-NOV-2004 (FIRST ENTRY)  
VV

XX DE XMYT 000 F.777 1 00044 4-3:

DE AXMI-008 full length coding vvv

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KW ss; gene; delta-endotoxin;

KW expression cassette; trans-

KW lepidoptera; coleoptera; f

KW pesticidal activity.

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PD 02-SEP-2004.

[illegible]

20-FEB-2004: 2004WQ-US00058

3E00S0-QM4007; 14007-BB1-02 11 XX

20-FEB-2003: 2003US-044863

PK Z0=FEF=2003; Z003US=044863  
 PP Z0=FEF=2003; Z003US=044863

PR Z0=FEB=2003; Z003US=044863  
 PR Z0=FEB=2003; Z003US=044870

PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
XX  
DR WFI; 2004-635574/61.  
DR P-PSDB; ADR89402.

XX New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.

XX  
PS Claim 1; SEQ ID NO 12; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.

Sequence 5980 BP; 2018 A; 976 C; 1146 G; 1840 T; 0 U; 0 Other;

|                       |                 |               |           |              |
|-----------------------|-----------------|---------------|-----------|--------------|
| Query Match           | 100.0%          | Score 2082;   | DB 13;    | Length 5980; |
| Best Local Similarity | 100.0%          | Pred. No. 0;  |           |              |
| Matches 2082;         | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;      |

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GTGAAAAGATGAGTCCATATCAAAATAAAAAATGAATATGAAATATTGGAAATCTCTCATCG   | 60  |
| Db | 168 | GTGAAAAGATGAGTCCATATCAAAATAAAAAATGAATATGAAATATTGGAAATCTCTCATCG   | 227 |
| Qy | 61  | AATAACACAATAACGCCAAACAGATATCTTTTGCAAAATAATCGGGATATGTCTACTATG     | 120 |
| Db | 228 | AATAACACAATAACGCCAAACAGATATCTTTTGCAAAATAATCGGGATATGTCTACTATG     | 287 |
| Qy | 121 | TCTTGGAATGATTGTTCAGGGAACTCATCGGATGAAATTTGGGAATCAGTCGGAACGATA     | 180 |
| Db | 288 | TCTTGGAATGATTGTTCAGGGAACTCATCGGATGAAATTTGGGAATCAGTCGGAACGATA     | 347 |
| Qy | 181 | ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTTAGTTTGGGTGGAAATTAAT   | 240 |
| Db | 348 | ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTTAGTTTGGGTGGAAATTAAT   | 407 |
| Qy | 241 | ACACTATTATCAATAATAGGAAACCTAATTCGACTAATCGTCAAACTGTGTGAGCACTT      | 300 |
| Db | 408 | ACACTATTATCAATAATAGGAAACCTAATTCGACTAATCGTCAAACTGTGTGAGCACTT      | 467 |
| Qy | 301 | TCCTATATGTGATTATTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAAGTGAT    | 360 |
| Db | 468 | TCCTATATGTGATTATTATCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTTAAAGTGAT    | 527 |
| Qy | 361 | GGGATTGCGAGATTTTGACGGGTAAATTGAAAAATATATAGAGAGTATTATCTTTCTTATCTTT | 420 |
| Db | 528 | GGGATTGCGAGATTTTGACGGGTAAATTGAAAAATATATAGAGAGTATTATCTTTCTTATCTTT | 587 |
| Qy | 421 | GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAAATTTCTGATATCGGACAA   | 480 |
| Db | 588 | GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAGACAAATAAATTTCTGATATCGGACAA   | 647 |
| Qy | 481 | TTAGTTTATTATTTTAAACCTTTTCAGAAAGAGATTTTCAATGAAATCTTAGAGAGGGTCATTG | 540 |
| Db | 648 | TTAGTTTATTATTTTAAACCTTTTCAGAAAGAGATTTTCAATGAAATCTTAGAGAGGGTCATTG | 707 |
| Qy | 541 | TCAGAGAAACAATGCTCAAGTATGTATTACCTACTTTTGGCACAACTCGCAATGTGCAG      | 600 |
| Db | 708 | TCAGAGAAACAATGCTCAAGTATGTATTACCTACTTTTGGCACAACTCGCAATGTGCAG      | 767 |
| Qy | 601 | TTATTACTATTAAAGGATGCAAGTTCATATTAAGACCAATGGTTCACATTTTTTGAGTGCA    | 660 |

Db 768 TTTATTACTAATAGGATGCAATTAATAAAGCAATGGTTCCATTTTGTAGTGA 827  
Qy 661 GAGAAATGTAAGATCGGAATTAATATCACTAACAGTGGTTGTGATTTTACCGGTGATTAC 720  
Db 828 GAGNATGTAAGATCGGAATTAATATCACTAACAGTGGTTGTGATTTTACCGGTGATTAC 887  
Qy 721 TATGACGATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATATGTTGATACAG 780  
Db 888 TATGACGATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATATGTTGATACAG 947  
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 840  
Db 948 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 1007  
Qy 841 AAATTTTCGTAGAGAAATGACGTTGGCGGTATTCGATATATTCGCTATATTCGCAACTTAT 900  
Db 1008 AAATTTTCGTAGAGAAATGACGTTGGCGGTATTCGATATATTCGCTATATTCGCAACTTAT 1067  
Qy 901 GATTTTGAGAAATATCCATTCGCAACACATGTAAGTGTGACTAGGGAATTTTATACAGAT 960  
Db 1068 GATTTTGAGAAATATCCATTCGCAACACATGTAAGTGTGACTAGGGAATTTTATACAGAT 1127  
Qy 961 GCAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAATTCGCTAATCTTTAAT 1020  
Db 1128 GCAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAATTCGCTAATCTTTAAT 1187  
Qy 1021 GCGTTAGAGGCTAATCGAAACACGGGACCTGGTTTACTTGGCTTAGCAAAATAGGT 1080  
Db 1188 GGGTTAGAGGCTAATCGAAACACGGGACCTGGTTTACTTGGCTTAGCAAAATAGGT 1247  
Qy 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTCGCTAATATGAA 1140  
Db 1248 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGCTGGGTAGGAACCTCGCTAATATGAA 1307  
Qy 1141 GACTACACAAGGGTAACGGTATTTTCAACGATGCTCTGGAACCTAGGATATGATCTA 1200  
Db 1308 GACTACACAAGGGTAACGGTATTTTCAACGATGCTCTGGAACCTAGGATATGATCTA 1367  
Qy 1201 CGTAATATGATTTTCAGAAATGCGATGTATATAAAATTTACTTCATTAGCTATCATGAAC 1260  
Db 1368 CGTAATATGATTTTCAGAAATGCGATGTATATAAAATTTACTTCATTAGCTATCATGAAC 1427  
Qy 1261 CTAGTAGGAGAGACTACCGCTAGACCAAGATGCTGTTTCAAAGGAGATTTTCGTAGG 1320  
Db 1428 CTAGTAGGAGAGACTACCGCTAGACCAAGATGCTGTTTCAAAGGAGATTTTCGTAGG 1487  
Qy 1321 GTAGGGGACCTGATTTAAATTTATGATGACAGGTAATAATGGGCTAAGCAGGATGACAAAT 1380  
Db 1488 GTAGGGGACCTGATTTAAATTTATGATGACAGGTAATAATGGGCTAAGCAGGATGACAAAT 1547  
Qy 1381 GAATCTACGTTCCACCTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440  
Db 1548 GAATCTACGTTCCACCTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1607  
Qy 1441 TCAAAATCGGCATGTGTTGTATATGGAACCTCCAGAGTTAACGTATATGTTTGGACACAT 1500  
Db 1608 TCAAAATCGGCATGTGTTGTATATGGAACCTCCAGAGTTAACGTATATGTTTGGACACAT 1667  
Qy 1501 ACAAGTTTAAACGTTGAAATATAATTTGAAGCCCAATCAAAATTACAAAATACCGCGGTG 1560  
Db 1668 ACAAGTTTAAACGTTGAAATATAATTTGAAGCCCAATCAAAATTACAAAATACCGCGGTG 1727  
Qy 1561 AAGAGTTTATTTACCTTCAAAATTTACTTGGCTAATGCTTATACCTATGTAATAAAGGCACCT 1620  
Db 1728 AAGAGTTTATTTACCTTCAAAATTTACTTGGCTAATGCTTATACCTATGTAATAAAGGCACCT 1787  
Qy 1621 CATACAGGTGGGATTTAATCCGTTTTTTTAAAGCAAAATCAGAGTATAACGAGTTTAT 1680  
Db 1788 CATACAGGTGGGATTTAATCCGTTTTTTTAAAGCAAAATCAGAGTATAACGAGTTTAT 1847  
Qy 1681 GCAGGTGCGGNAATTAGATTGATTATTAATAACAAAACCTCAGGACAAAGTTTACCGTATT 1740

Db 1848 GCAGGTGCGGNAATTAGATTGATTATTAATAACAAAACCTCAGGACAAAGTTACCGTATT 1907  
Qy 1741 CTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGATATCTTTTATCCAGAGGT 1800  
Db 1908 CTTTTTCGTTATGCTGCAGATAAAGCTGCTTTCTTTAGTGATATCTTTTATCCAGAGGT 1967  
Qy 1801 TGGGGTTCAAAATCGTTTTTGTATCGCTTGAAAATCTTACTCTGGAATATATGACGATTTA 1860  
Db 1968 TGGGGTTCAAAATCGTTTTTGTATCGCTTGAAAATCTTACTCTGGAATATATGACGATTTA 2027  
Qy 1861 AAATATAGTGAATTTTAAATTCGCTGAAATATCACACCTCCATTACCTAGTTCAAAACATT 1920  
Db 2028 AAATATAGTGAATTTTAAATTCGCTGAAATATCACACCTCCATTACCTAGTTCAAAACATT 2087  
Qy 1921 CAGATGGATGTGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAAACGTGGTTCTCGAC 1980  
Db 2088 CAGATGGATGTGAGATGCAAGCGAATAGTTTTTCAATCAGATGTAAAACGTGGTTCTCGAC 2147  
Qy 1981 AAAATTGAATTCCTCCCAAGTAATACAACTTTTAGAATATAGGGAGAACGGGACCTA 2040  
Db 2148 AAAATTGAATTCCTCCCAAGTAATACAACTTTTAGAATATAGGGAGAACGGGACCTA 2207  
Qy 2041 GAAAAACCAAGAACCGCGTGAACGATCTGTTTACCAATTAA 2082  
Db 2208 GAAAAACCAAGAACCGCGTGAACGATCTGTTTACCAATTAA 2249  
RESULT 3  
ADR89403  
ID ADR89403 standard; cdna; 2073 BP.  
XX  
AC ADR89403;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE AXMI-008 alternative start site coding sequence.  
XX  
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.  
OS Bacillus thuringiensis.  
XX  
FH Key  
FT 1. .2073  
FT CDS /tag= a  
FT /product= "Alternative AXMI-008"  
XX  
FN WO2004074462-A2.  
XX  
PD 02-SEP-2004.  
XX  
PF 20-FEB-2004; 2004WO-US005829.  
XX  
PR 20-FEB-2003; 2003US-0448632P.  
PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.  
PR 20-FEB-2003; 2003US-0448806P.  
PR 20-FEB-2003; 2003US-0448810P.  
PR 20-FEB-2003; 2003US-0448812P.  
PR 19-FEB-2004; 2004US-00781979.  
PR 19-FEB-2004; 2004US-00782020.  
PR 19-FEB-2004; 2004US-00782096.  
PR 19-FEB-2004; 2004US-00782141.  
PR 19-FEB-2004; 2004US-00782570.  
PR 19-FEB-2004; 2004US-00783417.  
XX  
PA (ATHE-) ATHENIX CORP.  
XX  
PI Carozzi N, Hargies T, Koziel MG, Duck NB, Carr B;  
XX WPI; 2004-635574/61.  
DR





Db 1741 TATGCTGCAGATAAAGCTGCTTCTTTAGTGATATCTTTATCCAGAGGTTGGGTTCA 1800  
Qy 1810 AATCGTTTTGTATCGCTTGAAAATCTTACTCTGGAAATATGACGATTTAAATATAGT 1869  
Db 1801 AATCGTTTTGTATCGCTTGAAAATCTTACTCTGGAAATATGACGATTTAAATATAGT 1860  
Qy 1870 GATTTAAATTCCTGAAATATACACCTCCATTAACCTAGTTTCAACATTCAGATGGAT 1929  
Db 1861 GATTTAAATTCCTGAAATATACACCTCCATTAACCTAGTTTCAACATTCAGATGGAT 1920  
Qy 1930 GTGAGATCAACGGAATAGTTTCAATCAGATGTAACCTGCTTCGCACAAAATTGAA 1989  
Db 1921 GTGAGATCAACGGAATAGTTTCAATCAGATGTAACCTGCTTCGCACAAAATTGAA 1980  
Qy 1990 TTCTCTCCCAAGTAATACAACTTTAGAAATATGAGGAGAACGGGACCTAGAAAAACA 2049  
Db 1981 TTCTCTCCCAAGTAATACAACTTTAGAAATATGAGGAGAACGGGACCTAGAAAAACA 2040  
Qy 2050 AGAAGCGGTGAACGATCTGTTTACCAATTAA 2082  
Db 2041 AAGAAGCGGTGAACGATCTGTTTACCAATTAA 2073

RESULT 4  
ADR89414  
ID ADR89414 standard; cDNA; 2019 BP.

AC ADR89414;  
DT 18-NOV-2004 (first entry)  
DE AXMI-008 coding sequence.  
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.

OS Bacillus thuringiensis.  
FH Key Location/Qualifiers  
FT CDS 1..2019  
FT /tag= a  
FT /product= "AXMI-008"  
FT /transl\_except= pos:1.. .3, aa:Met

XX WO2004074462-A2.  
XX  
XX  
XX 02-SEP-2004.  
XX  
XX 20-FEB-2004; 2004WO-US005829.  
XX  
XX 20-FEB-2003; 2003US-0448632P.  
XX 20-FEB-2003; 2003US-0448633P.  
XX 20-FEB-2003; 2003US-0448797P.  
XX 20-FEB-2003; 2003US-0448806P.  
XX 20-FEB-2003; 2003US-0448810P.  
XX 20-FEB-2003; 2003US-0448812P.  
XX 19-FEB-2004; 2004US-00781979.  
XX 19-FEB-2004; 2004US-00782020.  
XX 19-FEB-2004; 2004US-00782096.  
XX 19-FEB-2004; 2004US-00782141.  
XX 19-FEB-2004; 2004US-00782570.  
XX 19-FEB-2004; 2004US-00783417.  
XX (ATHE-) ATHENIX CORP.  
XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
XX WPI; 2004-635574/61.  
XX P-PSDB; ADR89415.  
XX

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.  
XX Claim 1; SEQ ID NO 26; 178pp; English.  
XX  
XX This sequence encodes an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.  
XX  
SQ Sequence 2019 BP; 662 A; 324 C; 419 G; 614 T; 0 U; 0 Other;

Query Match 35.9%; Score 747.2; DB 13; Length 2019;  
Best Local Similarity 69.8%; Pred. No. 9.9e-160;  
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

Qy 1 GTGAAAAAGATGAGTCCATATCAAAATATAAATGAATATGAATATTTGGAAATCTCATCG 60  
Db 1 GTGAAAAATATGAATCTTATCAAAATACAATGAATGAATATCTGGATGTTCCCG 60  
Qy 61 AATAACACAAATACGCCAAACAGATATCTTTTGGAAATATCGGGATATGCTACTATG 120  
Db 61 AATAACACAAATATGTCAACAGATATCTTTTGGAAAGGATCCAAATATATTTCTAT 120  
Qy 121 TCTTGGAAATGATTGTGAGGAAATCTATGGGATGAATTTGGAAATCAGTCGAAACGATA 180  
Db 121 AACCTGGACGCTGTGAGGAAAGGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATA 180  
Qy 181 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240  
Db 181 GTAACCTATTTGGGACATACCTTATACAAATCTTTGTAGAACCCGGTATAGTGGAAATTCCT 240  
Qy 241 ACACCTATATCAATATAGGAAACATTAATTCGACTAATTCGTCAAACTGTGTGAGCAGCT 300  
Db 241 GTAATATTTCAATATAATAAACAACTCAATTCGCTCTTCGTGCAATCTGTGTGAGCAGCT 300  
Qy 301 TCTATATGTGATTTTATATCTATAATTCGTAAGAGGTAGCCGATAGTCTTTTAAGTGAT 360  
Db 301 TCTATATGTGATTTAGTATCTATATATTCGTAAGAGGTAGACGAGCGTGTTAAGTGAC 360  
Qy 361 GCGATTGACAGATTTTGACGGTAAATTTGAAAAATATPAGAGATATATCTTTCTTATCTT 420  
Db 361 GGGGTTGCAGATTTTGAGGGTGAATGACTGCTTATCAAGATTAATATCTTCATTTATCTT 420  
Qy 421 GGGGCTTGCTTTAAGACCGGTAAACCACTTCAAAAGACAAATATCTGATATCGACAA 480  
Db 421 GAGGATTTGGCTTACAG-----ATNAATCAAAATCCCTAAAAAATCTGCTGAC 465  
Qy 481 TTAGTTTATTTATTTTAACTTTTCAAGAGAGATTTCAATGAAATTTCTAGGAGGTCATTG 540  
Db 466 GTAGTTTAAAGTTTCCAGCACGGGAGAGAGATTTCACTAACTTTTACAGGGTCATT 525  
Qy 541 TCAAGAAACAATGCTCAAGTATTTGTTATTAATCTTACTTTTGGCAAGCTCAAAATGTCAG 600  
Db 526 TCAAGACAGAAAGCTGAAATATTTATTTGCTACGTATGTGCAAGCTCAAAATGTCAT 585  
Qy 601 TTATTACTATTAGGGATCGACTTCAATATAAGCACAAATGTTCCCAATTTTGAAGTGA 660  
Db 586 TTATTACTATTAGGGACCGCTTAATAATAAAAAAGAAATGGGACCTAGTGTGTCACCG 645  
Qy 661 GAGNATGTAAGATCGGAATTAATATCACCTAACAGTGGTGTGTGATTTTCCCGTGATTAC 720



QY 61 AATAACACAAATACGCCAAACAGATATCCCTTTTGCAGAAATAATCGGGATATGCTCTACTATG 120  
DB 187 AATAACACAAATATGTCAACAGATATCCCTTTTGCAGAAAGATCAAAATATATTTCTCTAT 246  
QY 121 TCTTGGAAATGATGTGTCAGGGAACTCATGGATGAAATTTGGGAATCAGTCGGAACGATA 180  
DB 247 AACCTGGAGCCTTGTGAGGGAAGGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATA 306  
QY 181 ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAAT 240  
DB 307 GTAACCTATTGGGACATACCTTATACAATCTTCTGCTAGAACCCGGTATAGTGGAAATCTCT 366  
QY 241 AACTATATTCAATATAGGAACAACTAAATCCGACATAATCGTCAAACTGTCGTCAGCACTT 300  
DB 367 GTAATATTTTCAATATAAACAACTCAATCCCGTCTCTGGTCAATCTGGGAGCACTT 426  
QY 301 TCTATATGATTTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTCTTAAGTGAT 360  
DB 427 TCTATATGTGATTTAGTATCTATAATTCGTAAGAGGTAGACGAGAGCGGTGTTAAGTGAC 486  
QY 361 GCGATTTCGAGATTTTCAGCGGTAAATTGAAAAATTATAGAGAGTATTATCTTTCTTATCTT 420  
DB 487 GGGGTTGCAGATTTTCAGGGTGAATGACTGCTTATCAAGATTAATTAATCTTCATTAATCTT 546  
QY 421 GGGGCTTGGCTTAAAGACGGTAAACCACTTCAAAAAGACAAATAATCTGATATCGGACAA 480  
DB 547 GAGGATTTGGCTTACAG-----ATAAATCAATCCTAAAAAATCTGCTGAC 591  
QY 481 TTAGTTTATTTATTTTAACTTTTCAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCAATTC 540  
DB 592 GTAGTTTAAACAGTTTCAAGACACGGGAAGAGATTTTCACTAACTTTTAGCAGGGTCATTA 651  
QY 541 TCAAGAAACAAATGCTCAAGTATTTGTTATTAACCTTCTTTCACAAAGCTGCAAAATGTCAG 600  
DB 652 TCAAGACAGAACTGNAATATTAATTTGCTTACCTAGTAATGTGCAAGCTGCAATGTGCAT 711  
QY 601 TTATTAATAATTAAGGATGAGTTCATATAAAGCAACAATGTTTCCATTTTTCAGTGCA 660  
DB 712 TTATTAATAATTAAGGACGCGATTAATAATAAAGAAAGATTTGGGACAGTAGTGTCCACCG 771  
QY 661 GAGAATGTAGATCGGAATTAATATCACCTAACAGTGTGTGATTTTACCGGTGATTAC 720  
DB 772 TTGTATCCAGGTCAGGAGAA-----CTGATGT 801  
QY 721 TATGAGCGATTAATAATGCAAAACGGCAGAGTATACCAATTAATTTGTTATATTTGGTATCAG 780  
DB 802 AACGAGCGGTTAAAGCGGAAATAAAGAGTATACTAATTAATTTGTAGGGTGGTATAAC 861  
QY 781 GTAGGTTTAAATCAGATATAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTAAT 840  
DB 862 AAGGGTTTAGATCAGATACAGACAGGGGGGTACAAGTGTGCAAGTTTGGTCGAAATTAAT 921  
QY 841 AAATTTTCGTAGAAATGAGTTGGCGGTATTCGATATTAATCGCTATATTTCCAACTTAT 900  
DB 922 AAATTTTCGTAGAAATGAGTTGGCGGTATTCGATATTAATTCCTATATTTTCCAACTTAT 981  
QY 901 GATTTTCAGAAATATCCATTTGCCAACACATGTTAGAGTTGACTAGGGAATTTTATACAGAT 960  
DB 982 GATTTTGAATAATATCCATTTAGCAACAGGTGTAGAGTTAACTAGGGAATTTTATACAGAT 1041  
QY 961 GCAGTGGGATTTTCATCGGGAACTTATAGTTGGTTACGGAAATTTGGCCTAATCTTTTAAT 1020  
DB 1042 CCAGTGGGATTTTCAGGGGAAATTTATGGTTGGGAACGGTTTTT-----TTAGCTTTAAT 1095  
QY 1021 GGGTTAGAGCTAAATGGAACACGGGACCTGGTTTGTAGTTACTTGGCTTAGCBAATAGGT 1080  
DB 1096 TCGGTAGAGCAATGGAACACGGGACCTGGTTTGTAGTTACTTGGCTTCAAGCTATAGAT 1155  
QY 1081 ATATATAATGAGTATGTT-----TCGAGATATTTTTCGGGCTGGGTAGGAATCTCGT 1131  
DB 1156 ATATATAGTCTATTAATCTTTCAGCTTGGTTATCTTAGTGGCTGGGGGGAACCTCGT 1215

QY 1132 CATTATGAAGACTACACAAAGGGTAAACGGTATTTTTCACAGTATGCTCTGGAACCTAGAGT 1191  
DB 1216 CATTATGAAGACTTTCACAAAGGGTAAACGGTATTTTTCACAGTATGCTCTGGAACCTAGAGT 1275  
QY 1192 AATGATCTACGTAATAATTTGATTTTTCAGAAATGCGGATGATATAAAATTAATTTTTCATTAGCT 1251  
DB 1276 AATAATCCAGTAATAATTTATTTTGGCAATACCGATATATTTTAAATTAATTTTTCATTAGCT 1335  
QY 1252 A---TCATGAACCTAGTAGGAGAGACTACCGCTAGACACAGAGTATCGTGTTCCTCAAGGCA 1308  
DB 1336 AGATATGCAATGCAACCGCTTTGTTGGGTATTTCAATCCCAACGGCATCTTCTGTTTCAGTGCA 1395  
QY 1309 GATTTTTCGTAGGGTAGGGGACCTGATTTTAAATTAATGATGCAAGGTAAATATCGGCTAAGC 1368  
DB 1396 GAATTTTTCGACACACACTAAATACTTTTCTGTATGAGGTAAACAGTTTCTGGG---TAC 1452  
QY 1369 AGGATGACAATTTGAATCTACGTTCCCACTTGT-----ATTGCACCTCTAATCGTGTAGA 1422  
DB 1453 TCACAGACAAATTTGAATCTGTGTACAGGTATTAATAAGGATCTACCACTAGTCGTACA 1512  
QY 1423 GGACCTCTCTCATAGATTATCAAAATCGGCATGTGTGTATATGGAACCTCCAGAGTTAAC 1482  
DB 1513 AATTACTCTCATAGATTATCAAAATCGGCATGTGTTCAAATGAAACCTCCAGAGTTAAC 1572  
QY 1483 GTATATGTTGGACACATCAAGTTTAAACGTGAAATATATAATTTGAAGCCCAATCAAAAT 1542  
DB 1573 GTATTTGGTTGGACACATCAAGTATGAAAAAAGATAATCGAAATTTATCCAGATAAAAT 1632  
QY 1543 ACACAAATAACCGCGGTGAAGATTATTAACCTTCAAAATTAATCTTGTCTAATGCCATATACC 1602  
DB 1633 ACGAAATTCCTGCAAGTAAAGCTTTTGCCCTTACCAGCAGGTACAGGATATGCGAGAGT 1692  
QY 1603 TATGTAATAAAAGGCAC 1620  
DB 1693 TAGGTCACAGCTGGGCT 1710  
  
RESULT 6  
ADR89416  
ID ADR89416 standard; cdna; 2010 BP.  
XX ADR89416;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE AXMI-008 alternative start site coding sequence.  
KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
XX pesticial activity.  
OS Bacillus thuringiensis.  
XX  
FH Key Location/Qualifiers  
CDS 1..2010  
FT /\*tag= a  
FT /product= "Alternative AXMI-008"  
XX  
PN WO200407462-A2.  
XX  
PD 02-SEP-2004.  
XX  
PF 20-FEB-2004; 2004WO-US005829.  
XX  
PR 20-FEB-2003; 2003US-0448632P.  
PR 20-FEB-2003; 2003US-0448633P.  
PR 20-FEB-2003; 2003US-0448797P.  
PR 20-FEB-2003; 2003US-0448806P.  
PR 20-FEB-2003; 2003US-0448810P.  
PR 20-FEB-2003; 2003US-0448812P.  
PR 19-FEB-2004; 2004US-00781979.  
PR 19-FEB-2004; 2004US-00782020.

PR 19-FEB-2004; 2004US-00782096.  
 PR 19-FEB-2004; 2004US-00782141.  
 PR 19-FEB-2004; 2004US-00782570.  
 PR 19-FEB-2004; 2004US-00783417.  
 XX  
 PA (ATHE-) ATHENIX CORP.  
 XX  
 PI Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;  
 XX  
 DR WPI; 2004-635574/61.  
 DR P-PSDB; ADR89417.  
 XX  
 PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
 PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
 PT for producing organisms with pesticide resistance.  
 XX  
 PS Claim 1; SEQ ID NO 28; 178pp; English.  
 XX  
 CC This sequence encodes an isolated delta-endotoxin. Some of the delta-  
 CC endotoxin coding sequences of the invention have alternative start  
 CC codons, producing more than one protein from a single open reading frame.  
 CC The nucleic acid sequences of the invention are useful in DNA constructs  
 CC or expression cassettes for transformation and expression in plants and  
 CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
 CC killing lepidopteran or coleopteran pests. Compositions containing the  
 CC delta-endotoxins of the invention, and methods for their production, are  
 CC useful for the production of organisms with pesticide resistance,  
 CC specifically bacteria and plants. These organisms are useful for  
 CC generating altered or improved delta-endotoxin or delta-endotoxin-  
 CC associated proteins that have pesticidal activity, or for detecting the  
 CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
 CC nucleic acids in products or organisms.  
 XX  
 SQ Sequence 2010 BP; 657 A; 324 C; 417 G; 612 T; 0 U; 0 Other;  
 Query Match 35.5%; Score 739.8; DB 13; Length 2010;  
 Best Local Similarity 69.7%; Pred. No. 4.8e-158;  
 Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;  
 10 ATGAGTCCATATCAAAATAAATAATGAATATGAATATTTGGAAATCTCATCGAATAACACA 69  
 1 ATGAATTTCTTATCAAAATACAAATGAATATGAATATTTGGAAATCTCGAATATTTTCC 60  
 70 AATACGCCAAACAGATATCTTTTGCATTAATTCGGGATATGCTACTATGCTTCTGGAAT 129  
 61 AATATGTCAACAGATATCTTTTGCATTAATTCGGGATATGCTACTATGCTTCTGGAAT 120  
 130 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATACCAAGTAT 189  
 121 GCTTGTGAGGGAAGGCAATGGCAAGATACGTCGGGAATCAGTCGGATATAGTAATAT 180  
 190 GGGATTAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAATTAATACACTATTA 249  
 181 GGGACATACCTTATACAAATCTTGTGTAAGAACCGGTATAGGTGGAATCTCTGTAATAT 240  
 250 TCAATATAGGAACCTAATTCGATACCTAATCGTCAAACTGTGTGACACCTTCTATATGT 309  
 241 TCAATATTAACAAACTCAATCTCGTCTTCTGGTCAATCTGTGGCAGCCTTCTATATGT 300  
 310 GATTATATCTATAATTCGTAAGAGGTAGCCGATAGTGTGTTTAAGTGATGCGATTGCA 369  
 301 GATTATAGTATCTATATTCGTAAGAGGTAGACGAGCGGTGTAGTAGCGGGTTGCA 360  
 370 GATTTTGGCGGTAAATTTGAAAAATTATAGAGAGTATTTATCTTTCTTATCTTGGGCTTG 429  
 361 GATTTTGGCGGTAAATGACTGCTTATCAAGATTATTTATCTTATCTTGGAGATTGG 420  
 430 CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGCAATTAGTTTAT 489  
 421 CTTACAG-----ATNAATCAAAATCTTAAAAAACCTTGTGACGCTAGTTTAA 465  
 490 TATTTTAAACTTTTCAGAAAGAGATTTCAATGAATTTCTAGAGGGTCATTGTCAAGAAC 549

Db 466 CAGTTCACAGCAGCGGGAAGAGATTTCACTAAACTTTTAGCAGGGTCATTATCAAGACAG 525  
 Qy 550 AATGCTCAGATATGTTTATCTACTTTTGCACAGCTGCAAAATGTCGAGTATTTACTTA 609  
 Db 526 AAAGCTGAAATATATTTATGCTCAGTATGTGCAAGCTGCAAAATGTCGATTTACTTA 585  
 Qy 610 TTAAGGGATGCAAGTTCAATATATAAGCAAAATGTTTCCCAATTTTGTAGTCAGAGAAATGTA 669  
 Db 586 TTAAGGGACGAGTTAAATATATAAAGAAATGCGGACTAGTGTGCCACCGTTGTATCCA 645  
 Qy 670 AGATCGGAATTAATATCACTAACAGTGGTGTGTATTTTACCGGTGATTTACTATAGCGA 729  
 Db 646 GGGTCAGGAGAA-----CTGAATTTGAACGAGCG 675  
 Qy 730 TTAATAATGAAACCGCAGAGTATACCAATTTTGTATATTTGTTATGCTATCAGGTAGGTTTA 789  
 Db 676 TTAAGGCGAAATATAAGAGATATATAATTTGTAGGGTGGTATTAACAGGGTTTA 735  
 Qy 790 AATCAGATAAAAACAGGGGGGACAGGTCTGACACTTGGTCGAAATTTAATAAATTCGT 849  
 Db 736 GATCAGATAGACAGCGGGAACAGTGTGAAGTTTGGTCGAAATTTAATAAATTCGT 795  
 Qy 850 AGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCCAACTTATGATTTGAG 909  
 Db 796 AGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCCAACTTATGATTTGAA 855  
 Qy 910 AATATCCATTCGCAACACATGTAGATGACTAGGGAATTTATACAGATCAGATGCGGA 969  
 Db 856 AATATCCATTTAGCAACCAAGTGTAGATTAACCTAGGGAATTTATACAGATCAGTGGGA 915  
 Qy 970 TATTCATCGGGAACCTTATAGTTGGTTACGGAATTTGGCCCTAACTTTTATGGGTAGAG 1029  
 Db 916 TATTCAGGGGAAATTTATGGTTGGGAACGGTTT-----TTAGCTTTAATTCGGTAGAA 969  
 Qy 1030 GCTAATGGAACACGCGGACCTGTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT 1089  
 Db 970 GCAATGGAACACGCGGACCTGTTAGTTACTTGGCTTCAAGCTATAGATATATATAGT 1029  
 Qy 1090 GAGTATGTT-----TCGAGATATTTTGGCGCTGGGTAGGAACCTGCTATATGAA 1140  
 Db 1030 CATTCATTTAAATCTTCAGCTTATCTTAGTGGCTGGGGGGAACCTGCTATATGAA 1089  
 Qy 1141 GACTACACAAAGGGTAACGGTATTTTCAACGTATGCTCGGAACCTACGAGTAAATGATCTA 1200  
 Db 1090 GACTACAAAGGGTAACGGTCTTTTCAACGTATGCTCGGAACCTACGAGTAAATATCCA 1149  
 Qy 1201 CGTAATATTTGATTTTTCAGAAATCCGATGTATATAAATTTACTTCATTAGCTA---TCATG 1257  
 Db 1150 CGTAATATTTTGGCAATACCGATATATTTAAATTTTATTTCACTAGATAGATGCA 1209  
 Qy 1258 AACCTAGTAGGAGACTACCGCTAGACAGAGATTCGTGTTTCAAAGGACAGATTTTCGT 1317  
 Db 1210 ATGCAACCGTTTGTGGGTATTTCAATCCACCGCATCTTTGTTTCAGTGCAGAAATTTTT 1269  
 Qy 1318 AGGGTAGGGGACCTGATTTAAATTTATGATGAGGTAAATAATGGGCTAGCAGGATGACA 1377  
 Db 1270 CCGACACACTAAATATCTTCTGTAGAGGTAAACAGTTCCTGGG---TACTCA CAGACA 1326  
 Qy 1378 ATTGAATCTACGCTTCCCACTTGT-----ATTGCACTCTAAATGGGTGTAGAGGACCTCT 1431  
 Db 1327 ATTGAATCTGTGTACCAAGTATTAATAGGATCTACCACCTAGTCGTACAAATTAATCT 1386  
 Qy 1432 CATAGATTAATCAAAATCGGCAATGTTGTATATGGAACCTCCAGAGTTAACGATATATGTT 1491  
 Db 1387 CATAGATTAATCAAAATCGGCAATGTTTCAAAATGAAACCTCCAGAGTTAACGATATTTG 1446  
 Qy 1492 TCGACACATACAGTTTAAACCTGAAATATAATTTGAGCCCAATCAAAATTAACAAAAA 1551  
 Db 1447 TCGACACATACAGTTTAAACCTGAAATATAATTTGAGCCCAATCAAAATTAACAAAAA 1506  
 Qy 1552 CCGGGGTGAAGAGTTTATACCTTCAAAATTTATCTTGTAAATGCCTATATACCTATGTAATA 1611  
 Db 1507 CTTGCAAGTAAAGCTTTTGCCCTTCCACGAGGTACAGGATATGCAAGGAGTTACGTCACA 1566

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QY      1612 AAAGGCACT 1620
Db      1567 GCTGGCCCT 1575

RESULT 7
AAZ93234
ID      AAZ93234 standard; DNA; 1983 BP.
XX      AAZ93234;
AC
XX      04-JUL-2000 (first entry)
DT
XX      Sequence encoding truncated Cry9Aa toxin.
DE
XX      Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
KW      da.
XX
XX      Synthetic.
OS      Bacillus thuringiensis; ssp. galleria.
XX
XX      Key      Location/Qualifiers
FH      17..1966
FT      /*tag= a
FT      /product= "Cry9Aa toxin N-terminal fragment"
XX
XX      WO200011025-A1.
XX
XX      02-MAR-2000.
XX
XX      24-AUG-1999; 99NO-FI000698.
XX
XX      24-AUG-1998; 98FI-00001809.
XX
XX      (UNIC-) UNICROP LTD.
XX
XX      Kuvshinov V, Kanerva A, Koivu K, Pehu E;
XX
XX      WPI; 2000-224660/19.
DR      P-PSDB; AAY83039.
XX
XX      Modified synthetic DNA sequences comprise modification of the truncated
XX      cry9Aa gene of Bacillus thuringiensis for improved insect control in
XX      plants.
XX
XX      Claim 2; Page 55-57; 90pp; English.
XX
XX      Synthetic DNA sequences derived from the sequence of the truncated cry9Aa
XX      gene of Bacillus thuringiensis ssp. galleria can be used for the
XX      production of a unique insecticidal protein having the same properties as
XX      the N-terminal domain of the insecticidal protein encoded by the native
XX      cry9Aa gene of Bacillus thuringiensis ssp. galleria. The insecticidal
XX      toxin works by binding to specific receptor molecules in the gut of
XX      insects with consequent formation of ion channels in the epithelium. This
XX      action leads to ion efflux and paralysis of the intestinal function,
XX      which causes death of the insect. The synthetic DNA sequences exhibit
XX      enhanced expression through improved mRNA processing, stability, and/or
XX      translation providing improved tolerance against target insects. They can
XX      be used in the production of transgenic plants capable of expressing the
XX      N-terminal domain of the insecticidal protein encoded by the native
XX      cry9Aa gene. They therefore have a role in pest control and crop
XX      protection
XX
XX      Sequence 1983 BP; 626 A; 340 C; 387 G; 630 T; 0 U; 0 Other;
SQ
Query Match      8.2%; Score 170.2; DB 3; Length 1983;
Best Local Similarity 52.6%; Pred. No. 1.3e-28;
Matches 459; Conservative 0; Mismatches 363; Indels 51; Gaps 2;

QY      156 AATTGGGAATCAGTCGAACGATACAAAGTATGGGATAAAATCTTTATAGAGTTTGAT 215
Db      139 AATAGCGATGCGAGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 198

216 AGAACCTAGTTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAAACTAAT 269
    |||||
199 AGCACCTTCTCTTACTGGAATAATTTCAATAGTATATGACCTTATAGCTTAAGAGTAGTAGG 258
    |||||

QY      270 TCCGACTAATCGTCAAACTGTGTGTCAGCACTTTCTATATGTGATTTTATTTATCTATAATTCG 329
    |||||
259 AGGTAGTAGTGGACAAATCCATATCAGATTGTCTATATGTGACTTATTATCTATTATTGA 318
    |||||

QY      330 TAAAGAGGTAGCCGATAGTGTGTTTAAAGTGATGCGATTGCAGATTTTGAACGGTAATATGAA 389
    |||||
319 TTTACGGGTAACTCAGAGTGTGTTTAAATGATGGGATTCAGATTTTATGGTCTGTACT 378
    |||||

QY      390 AAATTATAGAGAGTATTATCTTTCTTATCTCTGGGCTTGGCTTAAAGACGGTAACCACT 449
    |||||
379 CTTATACAGGAATATTTAGAGGCTCTGGATAGCTGGAATAAGAAATCCTAATTTCTGCTTC 438
    |||||

QY      450 TCARAAGACAATAATCTGATATCGGACAATTAGTTTATTATTATTATAAATTTTCAGAAG 509
    |||||
439 TGCTGAAGAATCTCGTACTCGTTTGTAGAAATCGCCGACTCAGAAATTTGTAGAAATTTTAACT 498
    |||||

QY      510 AGATTTCAATGAAATTTCTAGGAGGTCATTTGTCAAGAAACAATGCTCAAGTATTGTTATT 569
    |||||
499 CCGAGGGTCTTTACGAATGGTGGCTCGTTAGTAGACAAATGCCCAATATTATTATT 558
    |||||

QY      570 ACCTACTTTTGCACAAGCTGCAAAATGTGCAGTATTACTATTAAAGGGATGAGTTCAATA 629
    |||||
559 ACCTTCTTTTGGAGCGCTGCAATTTTCCATTTATTACTACTAAGGGATGCTACTAGATA 618
    |||||

QY      630 TAAAGCACAAATGGTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689
    |||||
619 TGGCACTAATTGGGGGCTATACAATGCTACACCTTTTATAAATTATCAATCAAACTAGT 678
    |||||

QY      690 TAACAGATGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATCAAAAACGGCAGA 749
    |||||
679 AGAGCTTATT-----GAACT 693
    |||||

QY      750 GTATACCAATATTGTTTATATTGTTATCATGAGTGGTTTAAATCAGATAAAACAGGGGG 809
    |||||
694 ATATACTGATTTATTCGTCATCATTTGTTATAATCGAGGTTTCAACGAATTAAGACAGGAGG 753
    |||||

QY      810 GACAGGTCTGCACACTTCGTCGAAATTTAAATAATTTTCGTAGAGAAATGAGTTGGCGGT 869
    |||||
754 CACTAGTCTACAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGAGATGCAATTTGATGGT 813
    |||||

QY      870 ATTGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACA 929
    |||||
814 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTAACCAATAGAAACAGA 873
    |||||

QY      930 TGTAGAGTTGACTAGGGAATTTATACAGATGCGAGTGGGATATTTCATCGGGAACCTTATAG 989
    |||||
874 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAATTTGGTTTGTACATCGTAGTAGTCT 933
    |||||

QY      990 TTGGTTACGGAATGGCCCTAATCTATTTTAAATGG 1022
    |||||
934 TAGGGGAAAAGTTGGTTTACCTTTGTTAATAG 966
    |||||

RESULT 8
AAZ93235
ID      AAZ93235 standard; DNA; 3837 BP.
XX      AAZ93235;
AC
XX
XX      15-SEP-2003 (revised)
DT      04-JUL-2000 (first entry)
DE
XX      Sequence encoding native Cry9Aa toxin.
KW      Cry9Aa; insecticide; transgenic plants; pest control; crop protection;
XX      ds.
XX
XX      Bacillus thuringiensis; ssp. galleria.
OS

```



XX Key Location/Qualifiers  
 FH 385..2364  
 FT /\*tag= a  
 FT /product= "Cry9Aa toxin"  
 PN W0200011025-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 XX 24-AUG-1999; 99WO-F1000698.  
 PF  
 XX 24-AUG-1998; 98FI-00001809.  
 PR  
 XX (UNIC-) UNICROP LTD.  
 XX  
 XX Kuvshinov V, Kanerva A, Koivu K, Pehu E;  
 PI  
 XX WPI; 2000-224660/19.  
 DR P-PSDB; AAY82988.  
 XX  
 XX Modified synthetic DNA sequences comprise modification of the truncated  
 PT cry9Aa gene of *Bacillus thuringiensis* for improved insect control in  
 PT plants.  
 XX  
 XX Claim 10; Page 57-59; 90pp; English.  
 PS  
 XX Synthetic DNA sequences derived from the sequence of the truncated cry9Aa  
 CC gene of *Bacillus thuringiensis* ssp. *Galleria* can be used for the  
 CC production of a unique insecticidal protein having the same properties as  
 CC the N-terminal domain of the insecticidal protein encoded by the native  
 CC cry9Aa gene of *Bacillus thuringiensis* ssp. *Galleria*. The insecticidal  
 CC toxin works by binding to specific receptor molecules in the gut of  
 CC insects with consequent formation of ion channels in the epithelium. This  
 CC action leads to ion efflux and paralysis of the intestinal function,  
 CC which causes death of the insect. The synthetic DNA sequences exhibit  
 CC enhanced expression through improved mRNA processing, stability, and/or  
 CC translation providing improved tolerance against target insects. They can  
 CC be used in the production of transgenic plants capable of expressing the  
 CC N-terminal domain of the insecticidal protein encoded by the native  
 CC cry9Aa gene. They therefore have a role in pest control and crop  
 CC protection. (Updated on 15-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 3837 BP; 1279 A; 639 C; 791 G; 1128 T; 0 U; 0 Other;

Query Match 8.2%; Score 170.2; DB 3; Length 3837;  
 Best Local Similarity 52.8%; Pred. No. 1.6e-28;  
 Matches 459; Conservative 0; Mismatches 363; Indels 51; Gaps 2;

QY 156 AATTGGGAATCAGTCGNAACGATAACAAGTATTGGGATAAATCTTTATAGAGTTTCTGTAT 215  
 DB |||||  
 QY 216 AGAAGTATGTTGGGTGGGAATTAAATACATTTAT-----CAATAATAGGAAATTAAT 269  
 DB |||||  
 QY 597 AGCACCTTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTTATAGGTAAGTACTAGG 656  
 DB |||||  
 QY 270 TCGACTAATCGTCAACCTGTGTCAGCAGCTTCTATATGTGATTATTAATCTAATAATCG 329  
 DB |||||  
 QY 657 AGGTAGTAGTGGACAATCCATATCAGATTGTCTATATGTGACTTATATCTATTATTTGA 716  
 DB |||||  
 QY 330 TAAAGAGTAGCCGATAGTGTGTTTAAAGTGTGATGCGATTGTCAGATTTTGGCGTAAATTTGAA 389  
 DB |||||  
 QY 717 TTTACGGGTAGTCAGAGTGTGTTTAAATGATGGATTGCGAGATTTTAAATGTTCTGTACT 776  
 DB |||||  
 QY 390 AAATTATAGAGATTAATTTCTTTATCTTTGGGCTTGGCTTTAAAGACGGTAAACCACT 449  
 DB |||||  
 QY 777 CTTATACAGAACTATTTAGAGGCTCTGGATAGCTGGAATAAGAACTCTTAATCTGCTTC 836  
 DB |||||  
 QY 450 TCAAAAGACAATAATTTCTGATATCGGACAAATTAGTTTATTTATTTTAAACTTTTCAGAAAG 509  
 DB |||||  
 QY 837 TGCTGAAGAACTCCGCTACTCGTTTGTAGAAATCGCCGACTCAGAAATTTGATAGAAATTTAAC 896  
 DB |||||

QY 510 AGATTTCAATGAATTTCTAGAGGGTCATTTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569  
 DB |||||  
 QY 897 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCCAATATATTATTATT 956  
 DB |||||  
 QY 570 ACTTACTTTTGCACAAAGCTGCAAAATGTGCAAGTTATTACTATTAAAGGATGCAAGTTCAATA 629  
 DB |||||  
 QY 957 ACCTTCTTTTGGAGGGCTGCAATTTTCCATTTATTACTACTAAAGGATGCTACTAGATA 1016  
 DB |||||  
 QY 630 TAAAGCACAATGGTTCCTCCATTTTGTAGTCAGAGATGTAAGATCGGAATTTATATCAACC 689  
 DB |||||  
 QY 1017 TGGCATAATTTGGGGCTATACAATGCTACACCTTTATAAATTTATCAATCAAAATAGT 1076  
 DB |||||  
 QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGCGAGA 749  
 DB |||||  
 QY 1077 AGAGCTTATT-----GAACT 1091  
 DB |||||  
 QY 750 GTATACCAATTAATTTGTTTATATTTGATATCAGGTAGGTTTAAATTCAGATAAACAGGGGG 809  
 DB |||||  
 QY 1092 ATATACTGATTATTGGGTACATTTGGTATAATCGAGGTTTCAACGAACTAAGACAAGGAGG 1151  
 DB |||||  
 QY 810 GACAGTGTGACACCTTGGTCGAAATTTAAATTAATTTTCGTAGAGAAATGACGTTGGCGGT 869  
 DB |||||  
 QY 1152 CACTAGTGTACAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGAGATGACATTTGATGTT 1211  
 DB |||||  
 QY 870 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTTGCCAACACA 929  
 DB |||||  
 QY 1212 ATTAGATATAGTAGATCATTTTCAAGTCTTGATATTACTATTACCCAAATAGAAACAGA 1271  
 DB |||||  
 QY 930 TGTAGAGTTGACTAGGGAATTTATACAGATCAGTGGGATTTTCATCGGGAACCTTTATAG 989  
 DB |||||  
 QY 1272 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAAATTTGTTTGTATCATCGTAGTAGTCT 1331  
 DB |||||  
 QY 990 TTGGTTACGGAATTTGGCCTAAATCTTTAATCG 1022  
 DB |||||  
 QY 1332 TAGGGGAGAAAGTTGGTTTGGCTTTGTTAATAG 1364  
 DB |||||

RESULT 9  
 AAV16515  
 ID AAV16515 standard; DNA; 3471 BP.  
 AC AAV16515;  
 XX  
 XX 11-JUN-1998 (first entry)  
 XX  
 XX DNA encoding a *Bacillus thuringiensis* toxin designated 86BB1(a).  
 DE Toxin; lepidopteran pest; control; *Agrotis ipsilon*; black cutworm;  
 KW *Heliothis virescens*; *Helicoverpa zea*; ss.  
 KW  
 XX *Bacillus thuringiensis*.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3471  
 FT /\*tag= a  
 XX  
 XX W09800546-A2.  
 PN  
 XX 08-JAN-1998.  
 PD  
 XX 01-JUL-1997; 97WO-US011658.  
 PF  
 XX 01-JUL-1996; 96US-00674002.  
 PR  
 XX (MYCO ) MYCOGEN CORP.  
 PA  
 XX Schnepf HE, Wicker C, Narva KE, Walz M, Stockhoff BA;  
 PI  
 XX WPI; 1998-086971/08.  
 DR P-PSDB; AAW46856.  
 XX  
 PT New isolated *Bacillus thuringiensis* isolate(s) - used to obtain genes  
 encoding toxins which are active against lepidopteran pests such as the



```
Db 393 CTTATACAGAACTATTAGAGGCTCTGGATAGCTGGAATGAAGATCCTTAATCTCGTTC 452
Qy 450 TCAAGAGACAAATAATCTGATATCGGACAAATAGTTTATTATTATTTAAACTTTCAGAAAG 509
Db 453 TGTGAAGAACTCCGTACTCGTTTATGAATCGCGGACTCAGAAATTTGATAGAATTTTAAC 512
Qy 510 AGATTTCAATGAATTTCTAGGAGGTCATTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569
Db 513 CCGAGGCTCTTTAAAGATGGTGGCTCGTTAGCTAGACAAATGCCAAATATATTATT 572
Qy 570 ACTTACTTTTGCACAGCTGCAAAATGCGAGTTTATTACTATTAAAGGATGCGAGTTCAATA 629
Db 573 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTATTACTACTAAAGGATGCTACTAGATA 632
Qy 630 TAAAGCACATGCTTCCCATTTTGTAGTCAGAGAAATGAAGATCGGAATTAATATCACC 689
Db 633 TGGCACTAATTTGGGGCTATACAATGCTACACCTTTTATAAAATTTATCAATCAAACTAGT 692
Qy 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
Qy 750 GTATACAAATATTGTTTATTGTTATCGTATCAGTAGGTTTAAATTCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTATTGCGTACATTGGTATATATCGAGGTTTCAACGAACTAAGACAACGAGS 767
Qy 810 GACAGTGTCTGACACTTGTGCGAAATTAATAATTCGTAGAGAAATGACGTTGCGGT 869
Db 768 CACTAGTGTCTACAGCTTGTGTTAGAAATTCATAGATATCGTAGAGATGACATTTGATGT 827
Qy 870 ATTGGATATTATCGCTATATTCCAACTTATGTTTGGAGAAATATCCATGCGCACACA 929
Db 828 ATTAGAATAGTAGCATCTTTTCAAGTCTTGATATTACTAATTTACCCATAGAAACACA 887
Qy 930 TGTAGATGACTAGGGAATTTTATACAGATGCGAGTGGGATTTTCATCGGGAATTTATAG 989
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAATTTGGTTTGTACATCGTAGTAGTCT 947
Qy 990 TTGGTTACGAATTTGCGCTTAATACTTTTAAATGG 1022
Db 948 TAGGGAGAAAGTTGGTTAGCTTTTGTAAATAG 980
```

## RESULT 11

AAS02478  
ID AAS02478 standard; DNA; 2407 BP.

AC AAS02478;

XX 29-AUG-2001 (first entry)

DE B. thuringiensis DNA encoding a toxic crystal protein, Cry5T60.

XX Delta endotoxin; Lepidopteran-active; crystal protein; insecticide;  
KW transgenic plant; corn; wheat; soybean; oat; cotton; rice; rye; sorghum;  
KW sugarcane; tomato; tobacco; kapok; flax; potato; barley; turf grass;  
KW pasture grass; berry; fruit; legume; vegetable; ornamental plant; shrub;  
KW cactus; tree cell; gypsy moth; looper; tobacco budworm; spruce budworm;  
KW cotton leaf perforator; Cry5T60; ds.

OS Bacillus thuringiensis.

XX Key Location/Qualifiers  
FH 1. .2406  
CDS /tag= a  
FT /product= "Cry5T60"  
FT /partial  
FT /note= "No stop codon"

XX WO200119859-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US025361.  
PF  
XX 15-SEP-1999; 99US-0153995P.  
XX (MONS ) MONSANTO CO.  
XX  
XX Baum JA, Chu C, Donovan WP, Gilmer AJ, Rupar MJ;  
XX WPI; 2001-281518/29.  
DR P-PSDB; AAU02035.  
XX  
XX Lepidopteran-active Bacillus thuringiensis delta-endotoxin polypeptides  
XX and the polynucleotides that encode them, useful for increasing the  
XX insect resistance of plant.  
XX  
XX Claim 17; Page 127-128; 173pp; English.  
XX  
XX The sequence encodes a B. thuringiensis Lepidopteran-active delta-  
XX endotoxin, crystal protein Cry5T60. The Lepidopteran-active B.  
XX thuringiensis delta-endotoxin polypeptides may be used as compositions  
XX that are applied to plant crops to protect them from insect damage. The  
XX polynucleotides may be used in the production of transgenic plants that  
XX express the insecticidal polypeptides and consequently have improved  
XX insect resistance compared to non-transformed plants. Monocotyledonous or  
XX dicotyledonous plants may be protected in this way, for example corn,  
XX wheat, soybean, oat, cotton, rice, rye, sorghum, sugarcane, tomato,  
XX tobacco, kapok, flax, potato, barley, turf grass, pasture grass, berry,  
XX fruit, legume, vegetable, ornamental plant, shrub, cactus and/or tree  
XX cell. A wide range of insects (e.g. gypsy moth, looper, tobacco budworm,  
XX cotton leaf perforator and spruce budworm) may be affected by application  
XX of the insecticidal polypeptides (full details given in specification)  
XX  
XX Sequence 2407 BP; 785 A; 409 C; 495 G; 718 T; 0 U; 0 Other;

Query Match 7.7%; Score 160.6; DB 4; Length 2407;  
Best Local Similarity 51.9%; Pred. No. 2.1e-26;  
Matches 453; Conservative 0; Mismatches 369; Indels 51; Gaps 2;  
Qy 156 AATTTGGGAATCAGTCGAAACGATTAACAAGTATTTGGATAAATCTTTATAGATTTGTGAT 215  
Db 153 AATAGCGGATGCGCAAAAGAGCAGTATCTATTGGGACACCATAGTCTCTCTTATCAC 212  
Qy 216 AGAACCTAGTTTGGGTGGAAATTAATACACTATAT-----CAATATAGGAACATAAT 269  
Db 213 AGCACCTTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG 272  
Qy 270 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGTGATTTATTATCTATAATTCG 329  
Db 273 AGGTAGTAGTGACAAATCCATATCAGATTTGTCTATATGTGACTATTATCTATTATGA 332  
Qy 330 TAAAGAGGTAGCCGATAGTGTTTTAAAGTATCGGATTCGAGATTTTGACGGTAAATTTGAA 389  
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGATTCGAGATTTTAAATGTTCTGTACT 392  
Qy 390 AAATTTATAGAGATTTATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAAACCACT 449  
Db 393 CTTATACAGGAATCTTTTAGAGGCTCTGGATAGCTGGAATAAGAATCCTTAATTTCTGCTTC 452  
Qy 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATAGTTTATTATTATTATACTTTTCAAGAA 509  
Db 453 TGCTGAAGAACTCCGTACTCGTTTGTAGATCCCGGACTCAGAAATTTGATAGAAATTTAAC 512  
Qy 510 AGATTTCAATGAATTTCTAGGAGGTCATTTGTCAAGAAACAATGCTCAAGTATTTGTTATT 569  
Db 513 CCGAGGCTCTTTAAAGATGGTGGCTCGTTAGCTAGACAAATGCCAAATATATTATTATT 572  
Qy 570 ACTTACTTTTGCACAGCTGCAAAATGTCGAGTTTATTACTATTAAAGGATGCGAGTTCAATA 629  
Db 573 ACCTTCTTTTGCAGCGCTGCAATTTTCCATTTATTACTACTAAAGGATGCTACTAGATA 632  
Qy 630 TAAAGCACAAATGTTTCCCATTTTGTAGTCAGAGAAATGTAAGATCGGAATTTAATATCACC 689

633 TGGCACTAATTGGGGCTATACAATGCTACACTTTTATAATTAATCAATCAAACTAGT 592  
690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGA 749  
693 AGAGCTTATT-----GAACT 707  
750 GTATACCAATTATTTTATATATTTGTTATGTTATGTTTAAATCAGATAAACAGGGGG 809  
708 ATATAGTATGTTATTCGTATGTTGAGTAATCGAGTTCAACCGAACTAAGACAACGAGG 767  
810 GACAGTGTCTGACACTTGGTGCATAATTTAAATAATTTTCGTAGAGAAATGACGTTGGCGGT 869  
768 GCCTAGTGTACAGCTTGGTTAGATTTCATAGATATCGAGAGAGATGACATTGATGG 827  
870 ATTGATATATTCGTATATTTTCCAACTTATGATTGTTGAGAAATATCCATGCCAACACA 929  
828 ATTAGAAATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTAATACCAATAGAAACAGA 887  
930 TGTAGATTGACTAGGGAATTTATACAGATGCGATGCGATATTCATCGGGAATTATAG 989  
888 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAAATGGTTTGTATACATCGTAGTGTCT 947  
990 TTGGTTACGGAATTGGCCTAATACTTTTAATGG 1022  
948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

RESULT 12  
ABX13497  
ID ABX13497 standard; DNA; 4366 BP.  
XX AC ABX13497;  
XX DT 27-OCT-2003 (revised)  
XX DT 29-MAY-2003 (first entry)  
XX DE B. popilliae parasporal body-associated polynucleotide SEQ ID 19.  
XX KW Parasporal body; insect; larva; growth inhibiting; insecticidal;  
XX KW Scarabaeidae; turf; agricultural crop; tree; proteinaceous aggregate;  
XX KW Anomala cuprea; horticultural crop; gene; ds.  
XX OS Paenibacillus popilliae; subsp semadara.

XX FH Key Location/Qualifiers  
XX FT CDS 224..4258  
XX FT /\*tag= a  
XX FT /product= "parasporal body-associated protein"

XX PN US2002182693-A1.

XX PD 05-DEC-2002.

XX PF 12-APR-2002; 2002US-00120544.

XX PR 13-APR-2001; 2001JP-00115754.

XX PR 04-JUL-2001; 2001JP-00203463.

XX PA (DNIN ) DAINIPPON INK & CHEM INC.

XX PI Tanaka M, Yokoyama T, Aoyagi M, Hasegawa M, Ehara G, Kimura M;  
XX PI Nishinashi H;

XX DR WPI; 2003-328619/31.

XX DR P-PSDB; ABG74771.

XX PT New polypeptide having a larvae growth inhibiting or insecticidal effect  
XX PT in a Scarabaeidae insect, useful for controlling Scarabaeidae insect in  
XX PT turf, agricultural crops or trees.

XX PS Claim 12; Page 37-42; 54pp; English.

XX CC This invention describes a novel parasporal body-associated polypeptide

CC which has larval growth inhibiting or insecticidal effect in members of  
CC the Scarabaeidae insect family. The polypeptides and agents derived from  
CC the polypeptides of the invention are useful for controlling Scarabaeidae  
CC insects. Larvae of the Scarabaeidae insects eat the roots of a wide  
CC variety of plants e.g turf, agricultural or horticultural crops and  
CC trees, causing serious damage. This sequence encodes a polypeptide  
CC associated with the parasporal body contained in the sporangia of  
CC bacterium belonging to the Bacillus family. The parasporal body is a  
CC proteinaceous aggregate which comprises one kind or different kinds of  
CC polypeptides. The products of the invention have been shown to have a  
CC controlling effect on Anomala cuprea. (Updated on 27-OCT-2003 to  
CC standardise OS field)

XX SQ Sequence 4366 BP; 1383 A; 836 C; 976 G; 1171 T; 0 U; 0 Other;

Query Match 4.9%; Score 102.4; DB 8; Length 4366;  
Best Local Similarity 58.0%; Pred. No. 4.1e-13;  
Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

QY 716 ATTACTATGAGGGATTAAATGCAAAACGGCAGAGTATACCAATTAATTTTATATGCT 775  
DB 921 ATAATTACAATCGCCCAACAAAGGAACCTCCGCAACGTATGCAAAATCAITGTACAACCTGGT 980  
QY 776 ATCAGGTAGTGTTTAAATCAGATAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAAT 835  
DB 981 ATCAGACGGTTTACA-----AGATTGCAAGGAGCGATGCTAGCAGTTGGGTCNAAT 1034  
QY 836 TTAATAAAATTTGTTAGAGAAATGACGTTGGCGGTATTGATATATATCGCTATATTTCCAA 895  
DB 1035 ATAATCGATTTAGAAGAGAAATAACGTTAATAGTATTGATATTGTGCAATTTGTTTCAA 1094  
QY 896 CTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTATA 955  
DB 1095 ATTATGATGTTTCGTAGTTATCCAAATACAGTTACCGGAGAGCTTACGAGAGGAATTTATA 1154  
QY 956 CAGATGCGAGTGGGATATTATTCGGAACCTATAGTTGTTACGGAATTTGGCCTAATACCT 1015  
DB 1155 CGATCCAGCAGTATATAGCGGTACAGGTTCTATTCCTGTTGAGTCAAGCACCATCAT 1214  
QY 1016 TTAATGGTTTAGAGGCTAATGGAACACCGGGACCTGGTTTGTAGTTACTTGG 1065  
DB 1215 TTGCAGAAATAGAAAATATCGCAATTAGGGAACCAAGCAATTTTACTTTGG 1264

RESULT 13  
AEB90830  
ID AEB90830 standard; DNA; 4366 BP.

XX AC AEB90830;

XX DT 06-OCT-2005 (first entry)

XX DE Paenibacillus popilliae parasporal body gene SeqID19.

XX KW insecticide; crop improvement; plant insect pest; pesticide;

XX KW protein purification; gene; ds.

XX OS Paenibacillus popilliae.

XX FH Key Location/Qualifiers

XX FT CDS 224..4258

XX FT /\*tag= a

XX FT /product= "Bacillus popilliae parasporal body protein

XX FT SeqID20"

XX PN US2005172355-A1.

XX PD 04-AUG-2005.

XX PF 29-MAR-2005; 2005US-00091654.

XX PR 13-APR-2001; 2001JP-00115754.

XX PR 04-JUL-2001; 2001JP-00203463.

PR 12-APR-2002; 2002US-00120544.  
XX (DNIN ) DAINIPPON INK & CHEM INC.  
PA Tanaka M, Yokoyama T, Aoyagi M, Hasegawa M, Ehara G, Kimura M;  
PI Nishinashi H;  
XX  
XX WPI; 2005-563092/57.  
XX P-PSDB; AEB90831.  
XX  
XX New isolated polynucleotide encoding a protein having a larvae growth  
XX inhibiting or insecticidal effect on Scarabaeidae insects, useful as a  
XX controlling agent or insecticide against Scarabaeidae insects such as  
XX Anomala cuprea.  
XX  
XX Claim 28; SEQ ID NO 19; 53pp; English.  
XX  
XX This invention relates to a novel isolated polynucleotide and the encoded  
XX protein which has a larvae growth inhibiting or insecticidal effect on a  
XX Scarabaeidae insect. The invention may be useful for the development of  
XX compounds with an insecticide activity. The polypeptide encoded by the  
XX polynucleotide is useful as a larval growth inhibitor or insecticide  
XX against Scarabaeidae insects such as Anomala cuprea. The polypeptide can  
XX be applied to turf (for example golf courses), agricultural crops (for  
XX example sweet potato or peanuts), or trees. Larvae of Scarabaeidae  
XX insects such as Anomala cuprea, Blitopertha orientalis and Popillia  
XX japonica have conventionally been controlled by chemical pesticides, but  
XX as the larvae are buried in the ground large amounts of pesticide have to  
XX be used and there is a need for safer control methods. A polypeptide from  
XX Paenibacillus popilliae susp. melolonthae HI has a controlling effect on  
XX Melolontha melolontha (WO97/14798) but it was not made clear whether the  
XX bacterial strain and polypeptide have controlling effects on Anomala  
XX cuprea. Blitopertha orientalis and Popillia japonica. The invention  
XX provides new polypeptides obtained by screening Paenibacillus popilliae  
XX expression libraries using antisera obtained by immunizing animals with  
XX extracts of Paenibacillus popilliae species from infected Scarabaeidae  
XX larvae. The new polypeptides are unrelated to the previously identified  
XX polypeptide. Tests using the Escherichia coli clones identified in the  
XX library screening against Anomala cuprea larvae showed an inhibitory  
XX effect on the larvae. The present sequence is that of a gene of the  
XX present invention specific to the parasporal body region of Paenibacillus  
XX popilliae.  
XX  
XX Sequence 4366 BP; 1383 A; 836 C; 976 G; 1171 T; 0 U; 0 Other;  
SQ

Query Match 4.9%; Score 102.4; DB 14; Length 4366;  
Best Local Similarity 58.0%; Pred. No. 4.1e-13;  
Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

QY 716 ATTACTATGAGCGATTAAATGCAAAACGCGAGATATACCAATTATTGTTTATATGCT 775  
DB 921 ATATATCAATGCCAACAAAGGAATCCGCAACGATGCAATCATTTGACAACTTGT 980  
QY 776 ATCAGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAT 835  
DB 981 ATCAGACGGTTTACA-----AAGATTCAAGGCAGCGATGCTAGCAGTGGTCAATT 1034  
QY 836 TTAATTAATTCGTAGAGAAATGACGTTGGCGGTATTGATATATTCGTTATATTTCCAA 895  
DB 1035 ATAAATCGATTAGAGAGAAATAAACGTTAATAGTATTGATATTTGTCGATGTTTCAA 1094  
QY 896 CTTATGATTTGAGAAATATCAATTCGCAACACATGATGATGTTGACTAGGAAATTTATA 955  
DB 1095 ATTAGATGTTGTTAGTTATCAATACATACGTTACGGGGAGAGCTTAGAGAGAAATTTATA 1154  
QY 956 CAGATGCGAGTGGGATATTCATCGGAACTTATATGTTGTTACGGAATTCGCCATACATT 1015  
DB 1155 CGGATCCACAGTATATACGGGTACAGGTTCTTATTCCTGTTGAGTCAAGCACCATCAT 1214  
QY 1016 TTAATGGGTTAGAGGCTTAATGAACACGGGGACCTGGTTTGTAGTTACTTGG 1065  
DB 1215 TTGCAGAAATAGAAAATATCGCAATTTAGGGAACCAAGCAATTTTACTTGG 1264

RESULT 14  
ADR89411  
ID ADR89411 standard; cDNA; 1986 BP.  
XX  
XX AC ADR89411;  
XX  
XX DT 18-NOV-2004 (first entry)  
XX  
XX DE AXMI-009 alternative start site coding sequence #2.  
XX  
XX KW ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
XX expression cassette; transformation; transgenic; plant; bacteria;  
XX lepidoptera; coleoptera; pest; pesticide; resistance;  
XX pesticial activity.  
XX  
XX OS Bacillus thuringiensis.  
XX  
XX FH Key Location/Qualifiers  
XX FT 1..1986  
XX CDS /tag= a  
XX FT /product= "Alternative AXMI-009 #2"  
XX  
XX PN WO2004074462-A2.  
XX  
XX PD 02-SEP-2004.  
XX  
XX PF 20-FEB-2004; 2004WO-US005829.  
XX  
XX PR 20-FEB-2003; 2003US-0448632P.  
XX PR 20-FEB-2003; 2003US-0448633P.  
XX PR 20-FEB-2003; 2003US-0448797P.  
XX PR 20-FEB-2003; 2003US-0448806P.  
XX PR 20-FEB-2003; 2003US-0448810P.  
XX PR 20-FEB-2003; 2003US-0448812P.  
XX PR 19-FEB-2004; 2004US-00781979.  
XX PR 19-FEB-2004; 2004US-00782020.  
XX PR 19-FEB-2004; 2004US-00782096.  
XX PR 19-FEB-2004; 2004US-00782141.  
XX PR 19-FEB-2004; 2004US-00782570.  
XX PR 19-FEB-2004; 2004US-00783417.  
XX  
XX (ATHE-) ATHENIX CORP.  
XX  
XX PI Carozzi N, Hargies T, Kozziel MG, Duck NB, Carr B;  
XX  
XX DR WPI; 2004-635574/61.  
XX DR P-PSDB; ADR89412.  
XX  
XX PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
XX and polypeptides, useful for killing lepidopteran or coleopteran pests or  
XX PT for producing organisms with pesticide resistance.  
XX  
XX PS Claim 1; SEQ ID NO 23; 178pp; English.  
XX  
XX CC This sequence encodes an isolated delta-endotoxin. Some of the delta-  
XX endotoxin coding sequences of the invention have alternative start  
XX codons, producing more than one protein from a single open reading frame.  
XX The nucleic acid sequences of the invention are useful in DNA constructs  
XX or expression cassettes for transformation and expression in plants and  
XX bacteria. The nucleic acids and corresponding polypeptides are useful for  
XX killing lepidopteran or coleopteran pests. Compositions containing the  
XX delta-endotoxins of the invention, and methods for their production, are  
XX useful for the production of organisms with pesticide resistance,  
XX specifically bacteria and plants. These organisms are useful for  
XX generating altered or improved delta-endotoxin or delta-endotoxin-  
XX associated proteins that have pesticidal activity, or for detecting the  
XX presence of delta-endotoxin or delta-endotoxin-associated proteins or  
XX nucleic acids in products or organisms.  
XX  
XX SQ Sequence 1986 BP; 659 A; 310 C; 395 G; 622 T; 0 U; 0 Other;  
Query Match 4.8%; Score 99.6; DB 13; Length 1986;

Best Local Similarity 59.9%; Pred. No. 1.5e-12;  
Matches 187; Conservative 0; Mismatches 119; Indels 6; Gaps 1;  
QY 697 GGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGGCAGAGTATACC 756  
DB 619 GGTGATGATGAATTCGTGATATTTATATACAGACTACAAGGACTGATTAGAGATATATA 678  
QY 757 AATTATTGTTTATTTGCTATCAGGTAGGTTTAAATTCAGATAAAACAGGGGGGACAGGT 816  
DB 679 GATCATTGTATAAATCTTATAACACAGGCTTTAAATCAATTTAATC-----GCTCAAT 732  
QY 817 GCTGACACTGTCGAAATTTTAAATTTCTAGAGAAATGACGTTGCGGTATTTGAT 876  
DB 733 GCTCAAGATTGGGTGAGCTTTAATAGGTTTCGTACAGATATGACATTAACAGTATTAGAT 792  
QY 877 ATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAG 936  
DB 793 CTCGCAATATTTTCCAACTATGATCCAGTAGTATCCATTAGCAGTAAACCGGAA 852  
QY 937 TTGACTAGGAAATTTATACAGATGACGTGGGATATTCATCGGGAACCTTATAGTTGGTTA 996  
DB 853 TTGACTAGGAAATTTATACAGATCCAGTAGGCTTTACTGGGGTATTAGAAAGTGGAGGT 912  
QY 997 CGGAATTGGCCT 1008  
DB 913 AGGACTTACCCT 924

RESULT 15

ADR89409  
ID ADR89409 standard; cDNA; 2016 BP.

XX AC ADR89409;  
XX DT 18-NOV-2004 (first entry)

XX DE AXMI-009 alternative start site coding sequence.

XX ss; gene; delta-endotoxin; delta-endotoxin associate polypeptide;  
KW expression cassette; transformation; transgenic; plant; bacteria;  
KW lepidoptera; coleoptera; pest; pesticide; resistance;  
KW pesticidal activity.

XX OS Bacillus thuringiensis.

XX FH Key Location/Qualifiers  
FT CDS 1..2016  
FT /\*tag= a  
FT /\*product= "Alternative AXMI-009"

XX WO2004074462-A2.

XX 02-SEP-2004.

XX 20-FEB-2004; 2004WO-US005829.

XX 20-FEB-2003; 2003US-0448632P.

XX 20-FEB-2003; 2003US-0448633P.

XX 20-FEB-2003; 2003US-0448797P.

XX 20-FEB-2003; 2003US-0448806P.

XX 20-FEB-2003; 2003US-0448810P.

XX 20-FEB-2003; 2003US-0448812P.

XX 19-FEB-2004; 2004US-00781979.

XX 19-FEB-2004; 2004US-00782020.

XX 19-FEB-2004; 2004US-00782096.

XX 19-FEB-2004; 2004US-00782141.

XX 19-FEB-2004; 2004US-00782570.

XX 19-FEB-2004; 2004US-00783417.

(ATHE-) ATHENIX CORP.

XX Carozzi N, Hargiss T, Koziel MG, Duck NB, Carr B;

DR WPI; 2004-635574/61.  
XX P-PSDB; ADR89410.

PT New isolated delta-endotoxin and delta-endotoxin-associated nucleic acids  
PT and polypeptides, useful for killing lepidopteran or coleopteran pests or  
PT for producing organisms with pesticide resistance.

XX Claim 1; SEQ ID NO 21; 178pp; English.

XX This sequence encodes an isolated delta-endotoxin. Some of the delta-  
CC endotoxin coding sequences of the invention have alternative start  
CC codons, producing more than one protein from a single open reading frame.  
CC The nucleic acid sequences of the invention are useful in DNA constructs  
CC or expression cassettes for transformation and expression in plants and  
CC bacteria. The nucleic acids and corresponding polypeptides are useful for  
CC killing lepidopteran or coleopteran pests. Compositions containing the  
CC delta-endotoxins of the invention, and methods for their production, are  
CC useful for the production of organisms with pesticide resistance,  
CC specifically bacteria and plants. These organisms are useful for  
CC generating altered or improved delta-endotoxin or delta-endotoxin-  
CC associated proteins that have pesticidal activity, or for detecting the  
CC presence of delta-endotoxin or delta-endotoxin-associated proteins or  
CC nucleic acids in products or organisms.

XX Sequence 2016 BP; 668 A; 315 C; 400 G; 633 T; 0 U; 0 Other;

Query Match 4.8%; Score 99.6; DB 13; Length 2016;  
Best Local Similarity 59.9%; Pred. No. 1.5e-12;  
Matches 187; Conservative 0; Mismatches 119; Indels 6; Gaps 1;

QY 697 GGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGGCAGAGTATACC 756

DB 649 GGTGATGATGAATTCGTGATAATTTATATCAGACTACAAGGACTGATTAGAGATATATA 708

QY 757 AATTATTCTTTTATATTGCTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGACAGGT 816

DB 709 GATCATTGTATAACATTTCTATAACCCAGGGTTTAAATCAATTTAATC-----GCTCAAT 762

QY 817 GCTGACACTTGGTTCGAAATTTTAAATAATTCGTAGAGAAATGACGTTGCGGTATTTGGAT 876

DB 763 GCTCAAGATTGGGTGAGCTTTTAAATAGGTTTCGTACAGATATGACATTAAACAGTATTAGAT 822

QY 877 ATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAG 936

DB 823 CTCGCAATATTATTTTCCAACTATGATCCAGCTAGGTATCCATTAGCAGTAAAAACGGAA 882

QY 937 TTGACTAGGAAATTTTATACAGATGCGAGTGGGATTTTCATCGGGAACTTATAGTTGGTTA 996

DB 883 TTGACTAGGAAATTTTATACAGATCCAGTAGGTTTACTGGGGTATTAGAAAGTGGAGGT 942

QY 997 CGGAATTGGCCT 1008

DB 943 AGGACTTACCCT 954

Search completed: December 19, 2005, 14:37:55  
Job time : 777.097 secs



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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:48:03 ; Search time 1029.64 Seconds  
(without alignments)  
16721.276 Million cell updates/sec

Title: US-10-781-979-2

Perfect score:

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Scoring table: IDENTITY NUC

scoring cable: IDENTIII\_NOC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

2000 Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query |       |        |    | Description       |
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| 1          | 2082  | 100.0 | 2082   | 8  | US-10-781-979-2   |
| 2          | 2082  | 100.0 | 5980   | 8  | US-10-781-979-1   |
| 3          | 2073  | 99.6  | 2073   | 8  | US-10-781-979-4   |
| 4          | 747.2 | 35.9  | 2019   | 8  | US-10-782-141-2   |
| 5          | 747.2 | 35.9  | 2145   | 8  | US-10-782-141-1   |
| 6          | 739.8 | 35.5  | 2010   | 8  | US-10-782-141-4   |
| 7          | 168.6 | 8.1   | 3471   | 5  | US-10-099-285-71  |
| 8          | 160.6 | 7.7   | 2407   | 6  | US-10-428-961-29  |
| 9          | 102.4 | 4.9   | 4366   | 5  | US-10-120-544A-19 |
| 10         | 102.4 | 4.9   | 4366   | 10 | US-11-091-654-19  |
| 11         | 95.6  | 4.6   | 3687   | 7  | US-10-614-524-1   |
| 12         | 95.6  | 4.6   | 4173   | 6  | US-10-428-961-37  |
| 13         | 95.2  | 4.6   | 4359   | 5  | US-10-120-544A-3  |
| 14         | 95.2  | 4.6   | 4359   | 10 | US-11-091-654-3   |
| 15         | 94.4  | 4.5   | 1959   | 6  | US-10-428-961-5   |
| 16         | 93.4  | 4.5   | 3684   | 6  | US-10-428-961-62  |
| 17         | 93    | 4.5   | 1561   | 9  | US-10-687-879A-2  |
| 18         | 93    | 4.5   | 2019   | 7  | US-10-665-460A-1  |
| 19         | 93    | 4.5   | 2019   | 7  | US-10-665-460A-3  |
| 20         | 93    | 4.5   | 2019   | 7  | US-10-665-460A-5  |
| 21         | 93    | 4.5   | 2019   | 7  | US-10-665-460A-7  |
| 22         | 93    | 4.5   | 3471   | 5  | US-10-099-285-73  |
| 23         | 93    | 4.5   | 3471   | 6  | US-10-428-961-27  |

|    |      |     |      |    |                   |                   |
|----|------|-----|------|----|-------------------|-------------------|
| 24 | 93   | 4.5 | 4344 | 9  | US-10-687-879A-4  | Sequence 4, Appl  |
| 25 | 92.8 | 4.5 | 6930 | 3  | US-09-756-526A-1  | Sequence 1, Appl  |
| 26 | 92.8 | 4.5 | 6930 | 6  | US-10-345-020-1   | Sequence 1, Appl  |
| 27 | 92.8 | 4.5 | 6930 | 6  | US-10-342-821-1   | Sequence 1, Appl  |
| 28 | 91.4 | 4.4 | 4188 | 5  | US-10-120-544A-5  | Sequence 5, Appl  |
| 29 | 91.4 | 4.4 | 4188 | 10 | US-11-091-65A-5   | Sequence 5, Appl  |
| 30 | 89.2 | 4.3 | 1806 | 8  | US-10-782-020-4   | Sequence 4, Appl  |
| 31 | 89.2 | 4.3 | 1890 | 8  | US-10-782-020-2   | Sequence 2, Appl  |
| 32 | 89.2 | 4.3 | 2190 | 8  | US-10-782-020-1   | Sequence 1, Appl  |
| 33 | 88.2 | 4.2 | 3687 | 8  | US-10-809-953-9   | Sequence 9, Appl  |
| 34 | 88   | 4.2 | 2019 | 7  | US-10-665-460A-11 | Sequence 11, Appl |
| 35 | 87.8 | 4.2 | 1854 | 5  | US-10-032-717-33  | Sequence 33, Appl |
| 36 | 87.8 | 4.2 | 1854 | 5  | US-10-032-717-45  | Sequence 45, Appl |
| 37 | 87.8 | 4.2 | 1854 | 6  | US-10-414-637-33  | Sequence 33, Appl |
| 38 | 87.8 | 4.2 | 1854 | 6  | US-10-414-637-45  | Sequence 45, Appl |
| 39 | 87.8 | 4.2 | 1860 | 5  | US-10-032-717-19  | Sequence 19, Appl |
| 40 | 87.8 | 4.2 | 1860 | 6  | US-10-414-637-19  | Sequence 19, Appl |
| 41 | 87.8 | 4.2 | 1860 | 7  | US-10-606-320-15  | Sequence 15, Appl |
| 42 | 87.8 | 4.2 | 1860 | 8  | US-10-746-914-15  | Sequence 15, Appl |
| 43 | 87.8 | 4.2 | 1863 | 5  | US-10-032-717-29  | Sequence 29, Appl |
| 44 | 87.8 | 4.2 | 1863 | 5  | US-10-032-717-31  | Sequence 31, Appl |
| 45 | 87.8 | 4.2 | 1863 | 5  | US-10-032-717-41  | Sequence 41, Appl |

## ALIGNMENTS

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RESULT 1
US-10-781-979-2
; Sequence 2, Application US/10781979
; Publication No. US20040250311A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Koziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMT-008, A Delta-Endotoxin Gene and
; TITLE OF INVENTION: Methods for its Use
; FILE REFERENCE: 045600/274147
; CURRENT APPLICATION NUMBER: US/10/781,979
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,797
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2082)
US-10-781-979-2

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|    | Query Match           | 100.0%;  | Score 2082;  | DB 8;      | Length 2082; |
|----|-----------------------|--|--------------|------------|--------------|
|    | Best Local Similarity | 100.0%;  | Pred. No. 0; |            |              |
|    | Matches 2082;         | Conservative   | 0;           | Mismatches | 0; Indels    |
|    |                       |  |              |            | 0; Gaps      |
| Qy | 1                     | GTGAAAAGATGAGTCCATATCAAAATATAAAATGAATATGAAATATTGGAAATCTCTCATCG | 60           |            |              |
| Db | 1                     | GTGAAAAGATGAGTCCATATCAAAATATAAAATGAATATGAAATATTGGAAATCTCTCATCG | 60           |            |              |
| Qy | 61                    | AATAACACAATAACGCCAACAGATATCCTTTTGGCAAATAATCGGGATATGCTCTACTATG  | 120          |            |              |
| Db | 61                    | AATAACACAATAACGCCAACAGATATCCTTTTGGCAAATAATCGGGATATGCTCTACTATG  | 120          |            |              |
| Qy | 121                   | TCATTGGAATGATTGTGACGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA | 180          |            |              |
| Db | 121                   | TCATTGGAATGATTGTGACGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA | 180          |            |              |
| Qy | 181                   | ACAAGTATTGGGATAAATCTTTATAGAGTTTGTGATAGAACTTAGTTTGGGTGGAAATTAAT | 240          |            |              |

Db 181 ACAAGTATTGGGATAAATCTTATAGAGTTTGTGATAGAAACCTAGTTTGGGTGGAATTAAT 240  
Qy 241 ACACTATTATCAATAATAGGAAAACTTAATTCGCACTAATCGTCAAACTGTGTGACGACATT 300  
Db 241 ACACTATTATCAATAATAGGAAAACTTAATTCGCACTAATCGTCAAACTGTGTGACGACATT 300  
Qy 301 TCTATATGTGATTATTATCTATATTCGTAAGAGGTAGCCGATAGTGTCTTAAAGTGAT 360  
Db 301 TCTATATGTGATTATTATCTATATTCGTAAGAGGTAGCCGATAGTGTCTTAAAGTGAT 360  
Qy 361 GCGATTGACAGATTGTCAGCGTAAATGAAAAATTATAGAGAGTATTATCTTCTTATCTT 420  
Db 361 GCGATTGACAGATTGTCAGCGTAAATGAAAAATTATAGAGAGTATTATCTTCTTATCTT 420  
Qy 421 GGGGCTTGCTTTAAAGACGGTAAACCACTTCAAAAAGACAAATAATTCGATATCGGACAA 480  
Db 421 GGGGCTTGCTTTAAAGACGGTAAACCACTTCAAAAAGACAAATAATTCGATATCGGACAA 480  
Qy 481 TTAGTTTATATTTTAAACCTTTCAAGAGAGATTTCAATGAAATTCCTGATATCGGACAA 540  
Db 481 TTAGTTTATATTTTAAACCTTTCAAGAGAGATTTCAATGAAATTCCTGATATCGGACAA 540  
Qy 541 TCAAGAAAACAATGCTCAAGTATTGTTATTACCTACTTTTGGCAAGCTCAAAATGTGCAG 600  
Db 541 TCAAGAAAACAATGCTCAAGTATTGTTATTACCTACTTTTGGCAAGCTCAAAATGTGCAG 600  
Qy 601 TTATTACTATTAAAGGATCGAGTTCAATATAAAGCACAAATGGTCCCATTTTGGAGTGCA 660  
Db 601 TTATTACTATTAAAGGATCGAGTTCAATATAAAGCACAAATGGTCCCATTTTGGAGTGCA 660  
Qy 661 GAGAAATGTAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTTACCGGTGATAC 720  
Db 661 GAGAAATGTAAGATCGGAATTAATATACCTTAACAGTGGTGTGATTTTACCGGTGATAC 720  
Qy 721 TATGACCGATTAAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATTGGTATCAG 780  
Db 721 TATGACCGATTAAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATTGGTATCAG 780  
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 840  
Db 781 GTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 840  
Qy 841 AAATTTGTAAGATGAGTACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACTTAT 900  
Db 841 AAATTTGTAAGATGAGTACGTTGGCGGTATTGGATATTATCGCTATATTTCCAACTTAT 900  
Qy 901 GATTTTGAGAAATATCCATTGGCCAAACATGATAGAGTTGACATAGGGAATTTTATACAGAT 960  
Db 901 GATTTTGAGAAATATCCATTGGCCAAACATGATAGAGTTGACATAGGGAATTTTATACAGAT 960  
Qy 961 CGAGTGGGATATTCAATCGGAACTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAAT 1020  
Db 961 CGAGTGGGATATTCAATCGGAACTTATAGTTGGTTACGGAAATGGCCTTAATCTTTAAT 1020  
Qy 1021 GGGTTAGAGGCTAATGGAACAGGGGACCTGGTTAGTTTACTTGGCTTAGCAAAATAGGT 1080  
Db 1021 GGGTTAGAGGCTAATGGAACAGGGGACCTGGTTAGTTTACTTGGCTTAGCAAAATAGGT 1080  
Qy 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGTGGGTAGGAACCTCGTCAATATGAA 1140  
Db 1081 ATATATAATGAGTATGTTTCGAGATATTTTGGCGGTGGGTAGGAACCTCGTCAATATGAA 1140  
Qy 1141 GACTACAAAAGGGTAACGGTATTTTCAACGATATGCTGGAACCTACGAGTAATGATCTA 1200  
Db 1141 GACTACAAAAGGGTAACGGTATTTTCAACGATATGCTGGAACCTACGAGTAATGATCTA 1200  
Qy 1201 CGTAATATTGATTTTCAGAAATCCGATGATATAAAATTTACTTTCAAAAGGCAGATTTTCGTAG 1260  
Db 1201 CGTAATATTGATTTTCAGAAATCCGATGATATAAAATTTACTTTCAAAAGGCAGATTTTCGTAG 1260  
Qy 1261 CTAGTAGGAGAGACTACCGCTAGACCAGAGTATCGTGTGTTTCAAAAGGCAGATTTTCGTAG 1320  
Db 1261 CTAGTAGGAGAGACTACCGCTAGACCAGAGTATCGTGTGTTTCAAAAGGCAGATTTTCGTAG 1320

Qy 1321 GTAGGGGACCTGATTTAAATTTATGATGCAAGTAAATAATGGGCTAAGCAGGATGACAAATT 1380  
Db 1321 GTAGGGGACCTGATTTAAATTTATGATGCAAGTAAATAATGGGCTAAGCAGGATGACAAATT 1380  
Qy 1381 GAACTCTAGTTCCCACTTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440  
Db 1381 GAACTCTAGTTCCCACTTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTA 1440  
Qy 1441 TCAAAATCGGCATGTGTTGATATATGAAAATCCAGAGTTAACTGATATATGGTTGGACACAT 1500  
Db 1441 TCAAAATCGGCATGTGTTGATATATGAAAATCCAGAGTTAACTGATATATGGTTGGACACAT 1500  
Qy 1501 ACAAGTTTAAACCGTGAATAATTAATGAAAGCAATCAAAATTTACAAATACCGCGGTG 1560  
Db 1501 ACAAGTTTAAACCGTGAATAATTAATGAAAGCAATCAAAATTTACAAATACCGCGGTG 1560  
Qy 1561 AAGAGTTTAACTTCAAAATTTATCTGCTAATGCCTATACCTATGATATAAAGGCAT 1620  
Db 1561 AAGAGTTTAACTTCAAAATTTATCTGCTAATGCCTATACCTATGATATAAAGGCAT 1620  
Qy 1621 CATACAGGTGGGATTTAATCCGTTTTTAAAGAACAAAATCAGAGTATAAAGGCATTTAT 1680  
Db 1621 CATACAGGTGGGATTTAATCCGTTTTTAAAGAACAAAATCAGAGTATAAAGGCATTTAT 1680  
Qy 1681 GCAGGTGGCGAATTTAGATTGATTAATTAACAAAATCGCAGGACAAAGTTACCGTATT 1740  
Db 1681 GCAGGTGGCGAATTTAGATTGATTAATTAACAAAATCGCAGGACAAAGTTACCGTATT 1740  
Qy 1741 CGTTTTCTGTTATGCTGAGATAAAGCTGCTTTCTTTAGTGATATCTTTATCCAGAGGT 1800  
Db 1741 CGTTTTCTGTTATGCTGAGATAAAGCTGCTTTCTTTAGTGATATCTTTATCCAGAGGT 1800  
Qy 1801 TGGGTTTCAAAATCGTTTTGTTATCGCTTCAAAAATCTTACTCTGGAATTTATGACGATTTA 1860  
Db 1801 TGGGTTTCAAAATCGTTTTGTTATCGCTTCAAAAATCTTACTCTGGAATTTATGACGATTTA 1860  
Qy 1861 AAATATAGTATTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAATTT 1920  
Db 1861 AAATATAGTATTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAAAATTT 1920  
Qy 1921 CAGATGGATGCGAGATCAAGCGAATAGTTTTCATCAGATGTAAGCTGTTCTCGAC 1980  
Db 1921 CAGATGGATGCGAGATCAAGCGAATAGTTTTCATCAGATGTAAGCTGTTCTCGAC 1980  
Qy 1981 AAAATTGAATTCCTCCCAAGTAATAACAACTTTTAGAATATGAGGAGAACGGGACCTTA 2040  
Db 1981 AAAATTGAATTCCTCCCAAGTAATAACAACTTTTAGAATATGAGGAGAACGGGACCTTA 2040  
Qy 2041 GAAAAAACAAGAACCGGTGAACGATCTGTTTACCAATTTAA 2082  
Db 2041 GAAAAAACAAGAACCGGTGAACGATCTGTTTACCAATTTAA 2082

## RESULT 2

US-10-781-979-1  
; Sequence 1, Application US/10781979  
; Publication No. US20040250311A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
; FILE REFERENCE: 045600/274147  
; CURRENT APPLICATION NUMBER: US/10/781,979  
; PRIOR FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,797  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 5980
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-781-979-1

Query Match      100.0%; Score 2082; DB 8; Length 5980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGAAAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCG 60
Db 168 GTGAAAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCG 227

QY 61 AATAACACAATAACGCCAAACAGATATCCTTTTGGCAATAATCGGGATATGCTACTATG 120
Db 228 AATAACACAATAACGCCAAACAGATATCCTTTTGGCAATAATCGGGATATGCTACTATG 287

QY 121 TCTTGGAAATGATTTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATA 180
Db 288 TCTTGGAAATGATTTGTCAGGGAATCTCATGGATGAAATTTGGGAATCAGTCGAAACGATA 347

QY 181 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGAATTAAT 240
Db 348 ACAAGTATTTGGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGAATTAAT 407

QY 241 ACACTATTATCAATAATAGGAAACCTAATTCGCACTAATCGTCAAACTGTGTGAGCACCT 300
Db 408 ACACTATTATCAATAATAGGAAACCTAATTCGCACTAATCGTCAAACTGTGTGAGCACCT 467

QY 301 TCTATATGTGATTTATTTCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTAAAGTGAT 360
Db 468 TCTATATGTGATTTATTTCTATAATTCGTAAAGAGGTAGCCGATAGTGTTTAAAGTGAT 527

QY 361 GCGATTTCGAGATTTTGCAGGTAAATTTGAAATAATATAGAGATATATCTTCTTATCTT 420
Db 528 GCGATTTCGAGATTTTGCAGGTAAATTTGAAATAATATAGAGATATATCTTCTTATCTT 587

QY 421 GGGGCTTTGGCTTAAAGACGCTAAACCACTTCAAAAGCAAAATAATCTGATATCGGACAA 480
Db 588 GGGGCTTTGGCTTAAAGACGCTAAACCACTTCAAAAGCAAAATAATCTGATATCGGACAA 647

QY 481 TTAGTTTATTTATTTTAAACCTTTTCAAGAAAGATTTTCAATGAAATTTCTAGGAGGTCATTTG 540
Db 648 TTAGTTTATTTATTTTAAACCTTTTCAAGAAAGATTTTCAATGAAATTTCTAGGAGGTCATTTG 707

QY 541 TCAGAAACAAATGCTCAAGTATTTGTTATTAATCTTATTAATCTTTCGCAAGCTGCAATGTCAG 600
Db 708 TCAGAAACAAATGCTCAAGTATTTGTTATTAATCTTATTAATCTTTCGCAAGCTGCAATGTCAG 767

QY 601 TTATTTACTATTAAAGGATTCAGTTCAATATTAAGCACAAATGTTCCCATTTTGTAGTGCA 660
Db 768 TTATTTACTATTAAAGGATTCAGTTCAATATTAAGCACAAATGTTCCCATTTTGTAGTGCA 827

QY 661 GAGAAATGTAAGATTCGGAATTTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTAC 720
Db 828 GAGAAATGTAAGATTCGGAATTTAATATCACTTAACAGTGGTGTGATTTTACCGGTGATTAC 887

QY 721 TAGAGCGAATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATTAATGTTATCAG 780
Db 888 TAGAGCGAATTAATAATGCAAAACGGCAGAGTATACCAATTAATGTTTATTAATGTTATCAG 947

QY 781 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTGGTCGAATTTAAT 840
Db 948 GTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTGCTGACACTTGGTCGAATTTAAT 1007

QY 841 AAATTTTCGTAGAAATGAGCTTGGCGGTATTTGGATATTTATCGCTATATTTCCAACTTAT 900
Db 1008 AAATTTTCGTAGAAATGAGCTTGGCGGTATTTGGATATTTATCGCTATATTTCCAACTTAT 1067

QY 901 GATTTTGAATAATCCATTTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT 960
Db 1068 GATTTTGAATAATCCATTTGCCAACACATGTAGAGTTGACTAGGGAAATTTATACAGAT 1127
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961 GCAGTGGGATATTTCACTCGGGAACCTTATAGTTGGTTACGGAAATTTGGCCTAATCTTTTAAT 1020
1128 GCAGTGGGATATTTCACTCGGGAACCTTATAGTTGGTTACGGAAATTTGGCCTAATCTTTAAT 1187
1021 GGGTTAGAGGCTAATGGAACACGGGACCTGGTTTGTAGTTTACCTTGGCTTAGCAAAATAGGT 1080
1188 GGGTTAGAGGCTAATGGAACACGGGACCTGGTTTGTAGTTTACCTTGGCTTAGCAAAATAGGT 1247
1081 ATATATAATGAGTATGTTTTCGAGATATTTTTCGGGCTGGGTAGGAACTCGTCTATTATGAA 1140
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1141 GACTACACAAAGGTAACGCTATTTTCAACGATGCTGTGGAACTACAGAGTATGATCTA 1200
1308 GACTACACAAAGGTAACGCTATTTTCAACGATGCTGTGGAACTACAGAGTATGATCTA 1367
1201 CGTAATATTTGATTTTTCAGAAATCCGATGTATATAAAATTTACTTTCACTAGCTATCATGAAC 1260
1368 CGTAATATTTGATTTTTCAGAAATCCGATGTATATAAAATTTACTTTCACTAGCTATCATGAAC 1427
1261 CTAGTAGGAGAGACTACCCCTAGACAGAGTATCGTGTGTTTCAAAGCAGATTTTTCGTAGG 1320
1428 CTAGTAGGAGAGACTACCCCTAGACAGAGTATCGTGTGTTTCAAAGCAGATTTTTCGTAGG 1487
1321 GTAGGGGACCTGATTTTAAATTTATGATGCAAGGTAAATAATGGGCTAAGCAGGATGACAAAT 1380
1488 GTAGGGGACCTGATTTTAAATTTATGATGCAAGGTAAATAATGGGCTAAGCAGGATGACAAAT 1547
1381 GAATCTACGTTCCCACTTTGTATTTGCACTCTAAATGGTGTGTAGAGGACCTCTCATAGATTA 1440
1548 GAATCTACGTTCCCACTTTGTATTTGCACTCTAAATGGTGTGTAGAGGACCTCTCATAGATTA 1607
1441 TCAATTCGGGATGTTGTATATGGAACCTCAGAGTTAAACGTATATGTTGGTGGACACAT 1500
1608 TCAATTCGGGATGTTGTATATGGAACCTCAGAGTTAAACGTATATGTTGGTGGACACAT 1667
1501 ACAAGTTTAAACGTAATAATTAATGAAGCCAAATCAAAATACAAATACCGGCGGTG 1560
1668 ACAAGTTTAAACGTAATAATTAATGAAGCCAAATCAAAATACAAATACCGGCGGTG 1727
1561 AAAGATTATTAACCTTTCAAAATTTATCTGTAAATGCTTACCTATCTATGTAATAAAGGCACCT 1620
1728 AAAGATTATTAACCTTTCAAAATTTATCTGTAAATGCTTACCTATCTATGTAATAAAGGCACCT 1787
1621 CATACAGTGGGATTTAATTCGTTTAAAGAAACAAATCAGAGTATTAACGAGTTTAT 1680
1788 CATACAGTGGGATTTAATTCGTTTAAAGAAACAAATCAGAGTATTAACGAGTTTAT 1847
1681 GCAGGTGGCGGAATTTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTAT 1740
1848 GCAGGTGGCGGAATTTAGATTGATTATTAATAACAAACCTGCAGGACAAAGTTACCGTAT 1907
1741 CGTTTTTCGTTATGCTCGAGATAAAGCTGTTTTCTTTAGTGTATATCTTTATCCAGAGGT 1800
1908 CGTTTTTCGTTATGCTCGAGATAAAGCTGTTTTCTTTAGTGTATATCTTTATCCAGAGGT 1967
1801 TGGGTTTCAAAATCGTTTGTATCGCTTGAATAATCTTACTCTGGAAATTAAGACGATTTA 1860
1968 TGGGTTTCAAAATCGTTTGTATCGCTTGAATAATCTTACTCTGGAAATTAAGACGATTTA 2027
1861 AAATATAGTATTTTAAATTCGTCGAAATTTATCAACCTCCATTAACCTAGTTTCAACATTT 1920
2028 AAATATAGTATTTTAAATTCGTCGAAATTTATCAACCTCCATTAACCTAGTTTCAACATTT 2087
1921 CAGATGGATGTGGAGATGCAAGCAATAGTTTTTCAATCAGATGTAAACGTTCTTCGAC 1980
2088 CAGATGGATGTGGAGATGCAAGCAATAGTTTTTCAATCAGATGTAAACGTTCTTCGAC 2147
1981 AAAATTTGAATTCCTCCCAAGTAAATCAACAACTTTAGATAATATGAGGAGAAACGGACCTTA 2040
2148 AAAATTTGAATTCCTCCCAAGTAAATCAACAACTTTAGATAATATGAGGAGAAACGGACCTTA 2207
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QY 2041 GAAAAACAAAGACGCGGTGAACGATCTGTGTACCAATTAA 2082  
 DB 2208 GAAAAACAAAGACGCGGTGAACGATCTGTGTACCAATTAA 2249

## RESULT 3

US-10-781-979-4  
 ; Sequence 4, Application US/10781979  
 ; Publication No. US20040250311A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carozzi, Nadine  
 ; APPLICANT: Hargiss, Tracy  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Duck, Nicholas B.  
 ; APPLICANT: Carr, Brian  
 ; TITLE OF INVENTION: AXMI-008, A Delta-Endotoxin Gene and  
 ; FILE REFERENCE: Methods for Its Use  
 ; CURRENT APPLICATION NUMBER: US/10/781,979  
 ; CURRENT FILING DATE: 2004-02-20  
 ; PRIOR APPLICATION NUMBER: 60/448,797  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 2073  
 ; TYPE: DNA  
 ; ORGANISM: Bacillus thuringiensis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(2073)

## US-10-781-979-4

Query Match 99.6%; Score 2073; DB 8; Length 2073;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2073; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGAGTCCTATCAAAAATAAATAAGATGAATATTGGAATCTCTCATCGAATAACACA 69  
 DB 1 ATGAGTCCTATCAAAAATAAATAAGATGAATATTGGAATCTCTCATCGAATAACACA 60  
 QY 70 AATACGCCAAACAGATATCTTTTGCATAATATCGGATATCTCTATGTCCTTGGAAAT 129  
 DB 61 AATACGCCAAACAGATATCTTTTGCATAATATCGGATATCTCTATGTCCTTGGAAAT 120  
 QY 130 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCCGAAACGATAACAAGTATT 189  
 DB 121 GATTGTGAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCCGAAACGATAACAAGTATT 180  
 QY 190 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGGAATTAATACATATTA 249  
 DB 181 GGGATAAATCTTATAGAGTTTGTGATAGAACCTAGTTGGGTGGGAATTAATACATATTA 240  
 QY 250 TCAATAATAGGAAACTAATTCGTAATCCGCTAATCTCTCAACCTGCTCAGCCTTCTATATGT 309  
 DB 241 TCAATAATAGGAAACTAATTCGTAATCCGCTAATCTCTCAACCTGCTCAGCCTTCTATATGT 300  
 QY 310 GATTATTATCTATAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTGAATCGGATTGCA 369  
 DB 301 GATTATTATCTATAATTCGTAAGAGGTAGCGGATAGTGTGTTTAAAGTGAATCGGATTGCA 360  
 QY 370 GATTGTGAGGTAATTTGAAAAATTATAGAGAGTATTATCTTTCTTATCTTCGGGCTTGG 429  
 DB 361 GATTGTGAGGTAATTTGAAAAATTATAGAGAGTATTATCTTTCTTATCTTCGGGCTTGG 420  
 QY 430 CTTAAGAGCGTAAACCCCTTCAAGACAAATATCTTGATATCGGCAATTAGTTTAT 489  
 DB 421 CTTAAGAGCGTAAACCCCTTCAAGACAAATATCTTGATATCGGCAATTAGTTTAT 480  
 QY 490 TATTTTAAATCTTCAGAAAGAGATTTCAATGAAATCTTAGAGGGGTCAATTGTCAAGAAAC 549  
 DB 481 TATTTTAAATCTTCAGAAAGAGATTTCAATGAAATCTTAGAGGGGTCAATTGTCAAGAAAC 540

QY 550 AATGCTCAAGTATTGTTATTACTACTTTTGCACAAAGCTCAAAATGTGCAGTTATTACTA 609  
 DB 541 AATGCTCAAGTATTGTTATTACTACTTTTGCACAAAGCTCAAAATGTGCAGTTATTACTA 600  
 QY 610 TTAAGGGATCAGTTTCAATATATAAGACCAATGGTTCCTATTTTTCAGTGCAGAGATGTA 669  
 DB 601 TTAAGGGATCAGTTTCAATATATAAGACCAATGGTTCCTATTTTTCAGTGCAGAGATGTA 660  
 QY 670 AGATCGGAATTAATATACCTAAACAGTGGTGTGATTTTACCGGTGATTAATCATGAGGA 729  
 DB 661 AGATCGGAATTAATATACCTAAACAGTGGTGTGATTTTACCGGTGATTAATCATGAGGA 720  
 QY 730 TTAANAATCGAAACGGCAGAGTATACCAATTTATGTTTATATTTGTTATCGTATCAGTAGTTTA 789  
 DB 721 TTAANAATCGAAACGGCAGAGTATACCAATTTATGTTTATATTTGTTATCGTATCAGTAGTTTA 780  
 QY 790 AATCAGATATAAAGAGGGGGGACAGGTGCTGCACACTTGGTTCGAAATTTAAATAAATTCGT 849  
 DB 781 AATCAGATATAAAGAGGGGGGACAGGTGCTGCACACTTGGTTCGAAATTTAAATAAATTCGT 840  
 QY 850 AGAGAAATGACGTTGGCGGTATGGAATATATCGCTATATTTCCAACTTATGATTTGAG 909  
 DB 841 AGAGAAATGACGTTGGCGGTATGGAATATATCGCTATATTTCCAACTTATGATTTGAG 900  
 QY 910 AAATATCCATTTGCCAAACACATGTAGATTGACTAGGGAAATTTATACAGATGCAGTGGGA 969  
 DB 901 AAATATCCATTTGCCAAACACATGTAGATTGACTAGGGAAATTTATACAGATGCAGTGGGA 960  
 QY 970 TATTCATCGGAACTTATAGTTGGTTACGGAATTTGGCCTAATCTCTTTTAAATGGGTAGAG 1029  
 DB 961 TATTCATCGGAACTTATAGTTGGTTACGGAATTTGGCCTAATCTCTTTTAAATGGGTAGAG 1020  
 QY 1030 GCTAATGGAACAACGGGGACCTGGTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT 1089  
 DB 1021 GCTAATGGAACAACGGGGACCTGGTTAGTTACTTGGCTTAGCAAAATAGGTATATATAAT 1080  
 QY 1090 GAGTATGTTTCGAGATATTTTCCGGCTGGGTAGGAATCTGCTCATATTAGAAGCTACACA 1149  
 DB 1081 GAGTATGTTTCGAGATATTTTCCGGCTGGGTAGGAATCTGCTCATATTAGAAGCTACACA 1140  
 QY 1150 AAGGTAACGGTATTTTCAACGATGTCGGAATACGAGTAATGATCTACGTAATATT 1209  
 DB 1141 AAGGTAACGGTATTTTCAACGATGTCGGAATACGAGTAATGATCTACGTAATATT 1200  
 QY 1210 GATTTCAGAAATCCGATGTATATAAAATTTACTTTCATTAGCTATCATGAACCTAGTAGGA 1269  
 DB 1201 GATTTCAGAAATCCGATGTATATAAAATTTACTTTCATTAGCTATCATGAACCTAGTAGGA 1260  
 QY 1270 GAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGGAGATTTTCGTTAGGGTAGGGGA 1329  
 DB 1261 GAGACTACCGCTAGACAGAGTATCGTGTTCGAAAGGAGATTTTCGTTAGGGTAGGGGA 1320  
 QY 1330 CCTGATTTAAATTTATGATGAGGTAAATAATCGGCTTAAGCAGGATGACAAATTTGAATCTACG 1389  
 DB 1321 CCTGATTTAAATTTATGATGAGGTAAATAATCGGCTTAAGCAGGATGACAAATTTGAATCTACG 1380  
 QY 1390 TTCCCACTTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTATCAAAATGG 1449  
 DB 1381 TTCCCACTTGTATTGCACTCTAATGGTGTAGAGGACCTCTCATAGATTATCAAAATGG 1440  
 QY 1450 GCATGTGTTGATATGGAACCTCCAGAGTTAAACGTTAATGTTGGTGGACACATACAAGTTTA 1509  
 DB 1441 GCATGTGTTGATATGGAACCTCCAGAGTTAAACGTTAATGTTGGTGGACACATACAAGTTTA 1500  
 QY 1510 AAAAGTGAATATAAATTTGAAGCCAAATCAAAATTAACAAAATACCGCGGTGAAGATTAT 1569  
 DB 1501 AAAAGTGAATATAAATTTGAAGCCAAATCAAAATTAACAAAATACCGCGGTGAAGATTAT 1560  
 QY 1570 TACCTTCAAAATTTATCTTGTAAATGCTTATACCTATGTAATAAAGGCACTCATACAGGT 1629  
 DB 1561 TACCTTCAAAATTTATCTTGTAAATGCTTATACCTATGTAATAAAGGCACTCATACAGGT 1620  
 QY 1630 GGGGATTTAATCCCGTTTTTTTAAAGAACAAAATACAGATATAACGCGATTTATGCGAGGTGGC 1689

Db 1621 GGGGATTAATCCGTTTTTTAAGAACAAAATCAGAGTATAACGAGTTTATGCGAGTGC 1680  
Qy 1690 GGAATTAGATTGATTATTAATAACAAACATGCGAGGACAAAGTTACCGTATTTTCGTTTCGT 1749  
Db 1681 GGAATTAGATTGATTATTAATAACAAACATGCGAGGACAAAGTTACCGTATTTTCGTTTCGT 1740  
Qy 1750 TATGCTGCAGATAAAGTCGTTCTTTCTTTAGTGTATATCTTTATCCAGGAGGTTGGGGTTCA 1809  
Db 1741 TATGCTGCAGATAAAGTCGTTCTTTCTTTAGTGTATATCTTTATCCAGGAGGTTGGGGTTCA 1800  
Qy 1810 AATCGTTTTCTATCGTTGAAAAATCTTACTCTGGAATTTATGACGATTTAAATATAGT 1869  
Db 1801 AATCGTTTTCTATCGTTGAAAAATCTTACTCTGGAATTTATGACGATTTAAATATAGT 1860  
Qy 1870 GATTTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAACATTTTCAGATGGAT 1929  
Db 1861 GATTTTTAAATTCGCTGAAATTTATCACACCTCCATTTACCTAGTTCAACATTTTCAGATGGAT 1920  
Qy 1930 GTGGAGATCAAGCGAATAGTTTTCATCAGATGTAAACGTGGTTCTCGACAAAATTTGAA 1989  
Db 1921 GTGGAGATCAAGCGAATAGTTTTCATCAGATGTAAACGTGGTTCTCGACAAAATTTGAA 1980  
Qy 1990 TTCTCCCAAGTAATACAACTTTTGAATATGAGGAGAACCGGACCTAGAAAAAACA 2049  
Db 1981 TTCTCCCAAGTAATACAACTTTTGAATATGAGGAGAACCGGACCTAGAAAAAACA 2040  
Qy 2050 AAGAACCGGTGAACGATCTGTTTACCATTAA 2082  
Db 2041 AAGAACCGGTGAACGATCTGTTTACCATTAA 2073

## RESULT 4

US-10-782-141-2  
; Sequence 2, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargies, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; FILE OF INVENTION: Methods for Its Use  
; FILE REFERENCE: 045600/274143  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR APPLICATION NUMBER: 60/448,632  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2019)

US-10-782-141-2

Query Match 35.9%; Score 747.2; DB 8; Length 2019;  
Best Local Similarity 69.8%; Pred. No. 4e-160;  
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;  
Qy 1 GTGAAAAGATGAGTCCATATCAAAATAAATGAATATGAATATGGAATCCTCATCG 60  
Db 1 GTGAAAATATGAATTTCTTATCAAAATACAAATGAATATGAATATGGAATCCTCATCG 60  
Qy 61 AATAACAAAAATACGCCAACAGATATCTTTTGGCAAAATACCGGATATGCTACTATG 120  
Db 61 AATAACAAAAATATGCAACAGATATCTTTTGGCAAAATACCGGATATGCTACTATG 120  
Qy 121 TCTTGAATGATTGTTCAGGGAATCTCATGGGAATTTTGGGAATCAGTCGAAACGATA 180

Db 121 AACCTGCAGCGCTTGTTCAGGGAGGCCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 180  
Qy 181 ACAGATTATGGGATTAATCTTATAGAGTTTGTGATAGAACCTAGTTTGGGTGGAAATTAAT 240  
Db 181 GTAACTATTTGGGACATACCTTATACAAATCTTCTGTAGAACCCCGGTATAGGTGGAAATTCCT 240  
Qy 241 ACACATATATCAATAATAGGAAAACCTAAATCCGACCTAAATCGTCAAACTGTGTGACGACCTT 300  
Db 241 GTAAATATTTCAATATTAACAACTCATTTCCGTCTTCTGGTCAATCTGTGGGACGACCTT 300  
Qy 301 TCTATATGATGATTTATTTATCTATAATTCGTAAGAGGTAGCCGATAGTGTTTTAAGTGAT 360  
Db 301 TCTATATGATGATTTAGTATCTATAATTTCTGAAGAGGTAGACGAGAGCGGTGTTAAGTGAC 360  
Qy 361 GCGATTGCGAGATTTTACCGGTAAATTTGAAAATATATAGAGATTAATATCTTCTTATCTT 420  
Db 361 GGGGTTGCGAGATTTTGGGGTGAATGACTGCTTATCAAGATTAATATCTTCTATTTATCTT 420  
Qy 421 GGGGCTTGGCTTAAAGACGCTAAACCCACTTTCAAAAGACAAAATAATCTGATATCGGACAA 480  
Db 421 GAGGATTTGGCTTACAG-----ATTAATCAATCTTAAAAAATCTTGTGAC 465  
Qy 481 TTAGTTTATTTATTTTAAACTTTTCAAGAAAGAGATTTCAATGAAATTTCTAGGAGGTCAATG 540  
Db 466 GTAGTTTAAACAGTTTCAAGCAGCGGAAAGAGATTTTCACTAAACTTTTAGCAGGTCAATTA 525  
Qy 541 TCAAGAACAAATGCTCAAGTATTTTATTTACCTACTTTTGGCACAAGCTGCAAAATGTCAG 600  
Db 526 TCAAGACAGAAAGCTGAAATATTTATTTGCGCTACGTATGTGCAAGCTGCAAAATGTCAT 585  
Qy 601 TTATTACTATTAGGGATCGAGTTCAATATAAGCACAACTGTTCCCATTTTGTGAGTGA 660  
Db 586 TTATTACTATTAGGGACCGAGTTAAATATAAAGAAATGGGAGCTAGTGTGTCACCG 645  
Qy 661 GAGAATGTAGATCGGAATTAATATCACCTAAACAGTGGTTGTGATTTTACCGGTGATTAC 720  
Db 646 TTGTATCCAGGTCAGGAGAA-----CTGATGT 675  
Qy 721 TATGAGCGATTAATAATGCAAAACGGCAGAGATATACCAATTTATTTTATATGATGATCAG 780  
Db 676 AACGAGCGGTTAAAGACGAAAAATAAAGAGATGATCTAAATTTTGTGAGGTGGTATAAC 735  
Qy 781 GTAGGTTTAAATCAGATAAAACAGGGGACAGGTGCTGACACTTGGTCGAAATTTAAT 840  
Db 736 AAGGGTTTAGATCAGATAAAGACAGCGGCTACAGTCTGAAGTTTGGTCGAAATTTAAT 795  
Qy 841 AAATTTCTGAGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCCAACTTAT 900  
Db 796 AAATTTCTGAGAGAAATGACGTTGGCGGTATTTGGATATTTATTTGCTATATTTCCAACTTAT 855  
Qy 901 GATTTTGAGAAATATCCATTTGCCAACACATGTAGAGTTGACTAGGAAATTTATACAGAT 960  
Db 856 GATTTTGAAAAATATCCATTTAGCAACAAGTGTAGAGTTAACTAGGAAATTTATACAGAT 915  
Qy 961 GCAGTGGGATATTTATCCGGAACTTATAGTTCGTTACGGAATTTGGCCTAATCTTTAAT 1020  
Db 916 CCAGTGGGATATTTACGGGGAAATTTATGGTTGGGAAACGGTTTTT-----TTAGCTTTAAT 969  
Qy 1021 GGGTTAGAGGCTAATGGAACACCGGGACCTGGTTTGTAGTTTACTTGGCTTAGCAAAATAGGT 1080  
Db 970 TCGGTAGAGCAAAATGGAACACCGGGACCTGGTTTGTAGTTTACTTGGCTTCAAGCTATAGAT 1029  
Qy 1081 ATATATATAGTATGTT-----TCGAGATATTTTGGCGGTGGGTAGGAACTCGT 1131  
Db 1030 ATATATAGTCAATCTTATTAATCTTCAGCTTGGTTATCTTAGTGGCTGGGGGAACTCGT 1089  
Qy 1132 CATTATGAGACTACACAAAGGTAAACGGTATTTTCAACGTATCTCTGGAATCAGAT 1191  
Db 1090 CATTATGAGACTTCCAAAGGGTAAACGGTGTCTTTTCAACGTATCTCTGGAATCAGAT 1149  
Qy 1192 AATGATCTACGTAATATTTGATTTTTCAGAAATGCGGATGTATATAAATTTACTTTTAGCT 1251

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Db 1150 AATAATCCAGTAATATATATTTTGGCAATACCGATATATTTAAATATTTTCATTAGCT 1209
Qy 1252 A---TCATGAACCTAGTAGGAGAGACTACCGGTAGACCAAGATATCGTGTTCCTCAAAGGCA 1308
Db 1210 AGATATGCAATGCAACCGTTTGTGGGTATTCATCCACCGCATCTTGTTCACGTGCA 1269
Qy 1309 GATTTTCGTAGGTAGGGGACCTGATTTAAATATATGATGCAGGTAAATATGGCTAAGC 1368
Db 1270 GAATTTTTCCGACACACTAAATACCTTTCCTGTATGAGGTAAACAGTTCTGG---TAC 1326
Qy 1369 AGGATGACAATGAATCTACGTTCCCACTTGT-----ATTGCACCTCTAATGCTGTAGA 1422
Db 1327 TCACAGACAAATGNAATCTGTGTACCAAGGTATTAATAAGATCTACCACCTAGTCGTACA 1386
Qy 1423 GGACCTCTCATAGATATCAAAATGGCGCATGTGTGTATATGGAACCTCCAGAGTTAAC 1482
Db 1387 AATTAATCTCATAGATATCAAAATGGCGCATGTGTCAAAATGAAACCTCCAGAGTTAAC 1446
Qy 1483 GTATATGTTGACACATCAAGTTTAAACGTGAATATTAATTTGAAGCCCAATCAATTT 1542
Db 1447 GTATTTGGTGGACACATCAAGTATGAAAAAAGATTAATCGAATTTATCCAGATAAATTT 1506
Qy 1543 ACACAAATACCGCGGTGAAGGTATTAATACCTTCAAAATATCTTGCTAATGCCTATACC 1602
Db 1507 ACGCAATTCCTGCAGTAAAGCTTTTGCCTACCAGCAGGTACAGGATGCGAGAGT 1566
Qy 1603 TATGTAATAAAGGCACT 1620
Db 1567 TACGTACAGCTGGGCGCT 1584
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## RESULT 5

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US-10-782-141-1
; Sequence 1, Application US/10782141
; Publication No. US20040197917A1
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine
; APPLICANT: Hargiss, Tracy
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Duck, Nicholas B.
; APPLICANT: Carr, Brian
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
; FILE REFERENCE: Methods for Its Use
; CURRENT APPLICATION NUMBER: US/10/782,141
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,632
; PRIOR FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-782-141-1
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Query Match 35.9%; Score 747.2; DB 8; Length 2145;
Best Local Similarity 69.8%; Pred. No. 4.1e-160;
Matches 1143; Conservative 0; Mismatches 423; Indels 72; Gaps 7;

Qy 1 GTGAAAGATGAGTCCATATCAAAATAAAATGAATATGAATATTTGGAATCCTCATCG 60
Db 127 GTGAAATATGAAATCTTATCAAAATACAAATGAATATGAATATTTGGATGTTCCCG 186
Qy 61 AATAACAAAATACGCCAAACAGATATCTTTTGGAAATAATCGGGATATGCTACTATG 120
Db 187 AATAACAAAATATGTCAAAACAGATATCTTTTGGAAAGATCCAAATATATTTCTAT 246
Qy 121 TCTTGGATGATGTCAGGGAATCTCATGGGATGAAATTTGGGAATCAGTCGAAACGATA 180
Db 247 AACCTGGAGCTTGTGAGGGAAGGCCATGCGAAGATACGTGGGAATCAGTCTCGGATATA 306
Qy 181 ACAAGTATTTGGGATAAATCTTATAGATTTTGTGATAGAACCTAGTTTGGGTGGAATTAAT 240
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Db 307 GTAACCTATTTGGACATACCTTTATACAAATCTTGTAGAACCCGGTATAGGTGGAATTCCT 366
Qy 241 ACACCTATTATCAATAATAGGAAAACCTAATTCGGACTAATTCGTCAAATCGTGTGTCAGACATT 300
Db 367 GTAATATTTTCAATAATAAACAACTCATTCGGTCTTCTGGTCAATCTGTGGCAGACATT 426
Qy 301 TCTATATGTGATTTATATCTATTAATTCGTAAAGAGGTAGCCGATAGTGTGTTTAAAGTAT 360
Db 427 TCTATATGTGATTTAGTATCTATAATTCGTAAAGAGGTAGACGAGCGGTGTAAAGTGAC 486
Qy 361 GCGATTGCGAGATTTTGACGGTAAATTTGAAATATATAGAGATATATCTTCTTCTATCTT 420
Db 487 GGGGTTCGAGATTTTGGGGTGAATGACTGCTTATCAAGATTAATATCTTCAATTAATCTT 546
Qy 421 GGGGCTTCGCTTTAAAGACCGTAAACCACTTCAAAAGACAAATAAATCTCGATATCGGACAA 480
Db 547 GAGGATTCGCTTACAG-----ATAAATCAAAATCTTAAAAAACCTTGCTGAC 591
Qy 481 TTAGTTTATTAATTTTAAACTTTTCAGAAAGAGATTTCAATGAAAATTCCTAGGAGGTGATG 540
Db 592 GTAGTTAAACAGTTTCCAAGCAGCGGAAGAGATTTCACTAAACCTTTTAGCAGGGTCAITTA 651
Qy 541 TCAAGAAACAAATGCTCAAGTATTTGTTATCTACTTTTGCACAGCTGCAAAATGTCGAG 600
Db 652 TCAAGACAGAAAGCTGAAATATTAATTTGCTACGTATGTGCAAGCTGCAAAATGTGCAT 711
Qy 601 TTATTAATCTTAAAGGGATGCAAGTTCAATATATAAGCACAATGTTCCCAATTTTGTAGTGA 660
Db 712 TTATTAATCTTAAAGGACGAGTTAAATATTAAGAAAGATGCGGACTAGTGTGTCACCG 771
Qy 661 GAGAATGTAAAGTCGAAATTAATATCACTAACAGTGGTGTGATTTTACCGGTGATTAAC 720
Db 772 TTGTATCCAGGTTCAGGGAGAA-----CTGATTTGT 801
Qy 721 TATGAGCGATTAATAATGCAAAACGCGCAGAGTATACCAATTAATTTGTTATATTTGTTATCAG 780
Db 802 AACGAGCGGTATAAAGCGGAAATAAAGAGATATCTAATTAATTTGTTAGGTGTTATTAAC 861
Qy 781 GTAGGTTTAAATTCAGATAAAAAACAGGGGGGACAGGTGCTGACACTTGTGCGAAAATTAAT 840
Db 862 AAGGTTTATGATCAGATTAAGACAGCGGGTACAGTCTGTAAGTTTGTGCGAAAATTAAT 921
Qy 841 AAATTCGTAGAGAAATGACGTTCGCGGTATTTGATATATTCGTATATATTTCCAACTTAT 900
Db 922 AAATTCGTAGAGAAATGACGTTCGCGGTATTTGATATATTTGCTATATATTTCCAACTTAT 981
Qy 901 GATTTTGAGAAATATCCATTCGCAACACATCTAGAGTTGACTAGGAAATTTATACAGAT 960
Db 982 GATTTTGAAAAATATCCATTTAGCAACAGGTGTAGAGTTAACTAGGGAATTTATACAGAT 1041
Qy 961 GCAGTGGGATATTCATTCGGGAACCTTATAGTTGGTTACGGAATTTGGCCTAAATCTTTTAAT 1020
Db 1042 CCAGTGGGATATTCAGGGGAAATTTGTTGGGAACGGTTTT-----TTAGCTTTAAT 1095
Qy 1021 GGGTTAGAGGCTAATGGAACACCGGGACCTCGTTTGTAGTTACTTGGCTTTAGCAAAATAGGT 1080
Db 1096 TCGGTAGGAAGCAAAATGGAACACCGGGACCTCGTTTGTAGTTACTTGGCTTTCAAGCTATAGAT 1155
Qy 1081 ATATATATGAGTATGTT-----TCGAGATATTTTGGCGGTGGGTAGGACTCGT 1131
Db 1156 ATATATGCTCAATCTTATTAATCTTCAGCTTGGTTTCTTAGTGGCTGGGGGGAACTCGT 1215
Qy 1132 CATTTATGAAGACTACACAAAGGGTAACCGTATTTTCAACGTATGCTGGAACCTACGAGT 1191
Db 1216 CATTTATGAAGACTTCAAAAGGGTAACCGTCTTTTCAACGTATGCTGGAACCTACGAGT 1275
Qy 1192 AATGATCTAGTAAATATTTGATTTTTCAGAAATGCCGATGATATAAAATTTACTTTCAATGCT 1251
Db 1276 AATAATCCACGTAATATTTATTTTGGCAATACCGGATATATTTTAAATATTTTCAATGCT 1335
Qy 1252 A---TCATGAACCTTAGTAGGAGAGACTACCGCTAGACCAGAGATATCGTGTGTTTCAAAGGCA 1308
```



Db 1336 AGATATGCAATGCAACCGTTTGTGGGTATTCATCCACGGCATCTGTGTTTCCAGTGCA 1395  
QY 1309 GATTTTCGTAGGTAGGGGACCTGATTTAAATATGATGCTAGGTAAATATGAGTGGCTAAGC 1368  
Db 1396 GAATTTTTCGACACACTAAATATCTTCTCTGTATGAGGTAAACAGTTCTTGGG---TAC 1452  
QY 1369 AGGATGACAAATGAAATCTACGTTCCCACTTGT-----ATTGCACCTTAATGTTGTAGA 1422  
Db 1453 TCACAGACAATTGAATCTGTGTTTACCAGGTATTAATAAGGATCTACCACTAGTCGTACA 1512  
QY 1423 GGACCTCTCATAGATATCAAAATGCGGCATGTGTTGTATATGGAACCTCCAGAGTTAAC 1482  
Db 1513 AATTACTCTCATAGATATCAAAATGCGGCATGTGTTTCAAAAATGAAACCTCCAGAGTTAAC 1572  
QY 1483 GTATATGTTGGACACATACAAGTTTAAACCGTGAATAATATTCGAAGCCCAATCAAAAT 1542  
Db 1573 GTATTTGTTGGACACATACAAGTATGAAAAAAGATAATCGAAATTTATCCAGATAAAAT 1632  
QY 1543 ACACAAAATACCGCGGTGAAGCTTATTACCTTCAAAAATTAATCTTCTTAATGCTTATACC 1602  
Db 1633 AGCAAAATTCCTGCACTAAAGCTTTTGGCCTACACAGCGGTACAGGATATGCAGGAGT 1692  
QY 1603 TATGTAATAAAGGCACT 1620  
Db 1693 TACGTACAGCTGGGCT 1710

## RESULT 6

US-10-782-141-4  
; Sequence 4, Application US/10782141  
; Publication No. US20040197917A1  
; GENERAL INFORMATION:  
; APPLICANT: Carozzi, Nadine  
; APPLICANT: Hargiss, Tracy  
; APPLICANT: Kozziel, Michael G.  
; APPLICANT: Duck, Nicholas B.  
; APPLICANT: Carr, Brian  
; TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and  
; FILE REFERENCE: Methods for Its Use  
; CURRENT APPLICATION NUMBER: US/10/782,141  
; CURRENT FILING DATE: 2004-02-20  
; PRIOR FILING DATE: 2003-02-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 2010  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2010)  
US-10-782-141-4

Query Match 35.5%; Score 739.8; DB 8; Length 2010;  
Best Local Similarity 69.7%; Pred. No. 2e-158;  
Matches 1135; Conservative 0; Mismatches 422; Indels 72; Gaps 7;  
QY 10 ATGAGTCCATATCAAAATGAAATGAAATATGAAATATGGAATCTCTCATCGAATAACACA 69  
Db 1 ATGAATTTCTTATCAAAATCAAAATGAAATGAAATATGAAATCTCTCGATGTTCCCGAATAACACA 60  
QY 70 AATACGCCAACAGATATCTTTTGGCAATAATATCGGGATATGTTACTATGTTCTTGGAAAT 129  
Db 61 AATATGTCAACAGATATCTTTTGGCAAGGATCCAAATATATTTCTTATTAACCTGGAC 120  
QY 130 GATTGTGCGGAATCTCATGGATGAAATTCGGAAATCAGTCGAAACGATACAGTATT 189  
Db 121 GCTTGTGCGGAAGGCCATGGCAAGATACGTGGGAATCAGTCTCGGATATAGTAATATT 180  
QY 190 GGGATAAATCTTATAGATTTGTGATAGAACCTAGTTTGGGTGGAATTAATACATTTA 249

Db 181 GGGACATACCTTTATACAAATCTTGTAGAACCCGGTATAGGTGGAATTCCTGTAATATTT 240  
QY 250 TCAATATATAGGAAAATAATTCGGACTAATTCGTCAAACTGTGTAGCACTTTTCTATATGT 309  
Db 241 TCAATAATAAACAACCTCAATTCCTGCTCAATTCGTGTCATCTGTGCGCAGCACTTTTCTATATGT 300  
QY 310 GATTTTATATCTATAATTCGTAAAGAGGTAGCCGATAGTGTGTTTAAAGTACATGCGATTGCA 369  
Db 301 GATTTAGTATCTATAATTCGTAAAGAGGTAGACGAGCGGTGTTAAGTACGCGGGTTGCA 360  
QY 370 GATTTTGACGGTAAATTTGAAAAATATATAGAGAGTATTAATCTTTTCTTATCTCTGCGGCTTGG 429  
Db 361 GATTTTGAGGGTGAATGACTCTTATCAAGATTAATATCTTCAATTTATCTTCTGAGGATGCG 420  
QY 430 CTTAAAGACGGTAAACCACTTCAAAAGACAAATAATCTTGATATCGGACAAATAGTATTAT 489  
Db 421 CTTACAG-----ATAAATCAAAATCTTAAAAAACTTGTCTGACGCTAGTTTAA 465  
QY 490 TATTTTAAACTTTTCAAAAAGAGATTTCAATGAAATTTCTAGGAGGGTCAATTTGTCAAGAAAC 549  
Db 466 CAGTTTCCAAGCAGCGGAAGAATTTTCACTAAATCTTTTAGCAGGGTCAATTTCAAGACAG 525  
QY 550 AATGCTCAAGTATGTTTATTAATCTACTTTTGCACAAGCTGCAAAATGTCAGTATTACTA 609  
Db 526 AAAGCTGAAATATTTATTTGCTAGCTATGTCAGCTGCAAAATGTCGCAATTTTATTA 585  
QY 610 TTAAGGGATGCAAGTTCAATATATAAGCACAATGTTCCCAATTTTGTAGTCCAGAGAATGTA 669  
Db 586 TTAAGGGACGCAAGTTAAATATATAAAGAAATGCGGCACTAGTGTGTCACCGTTGTATCCA 645  
QY 670 AGATCGGAATTAATATATCACTAACAGTGTGTTGATTTTACCGGTGATTAATCTATGAGCGA 729  
Db 646 GGGTCAGGGAGAA-----CTGATTTGAACGAGCGG 675  
QY 730 TTAATAATGCAAAACGCGCAGAGTATACCAATTAATGTTTATATGTTGATCAGGTAGGTTTA 789  
Db 676 TTAATAAGCGAAAATAAAGAGTATTAATTAATTTGTTAGGTGTTTAAACAAGGGTTTA 735  
QY 790 AATCAGATAAACAAGCGGGGAGCAGTGTCTGACACATCTGTCGAAATTTAATAAATTTTCGT 849  
Db 736 GATCAGATAAAGACAGCGCGGTAACAAGTGTGTAAGTTTGTGCGAAATTTAATAAATTTTCGT 795  
QY 850 AGAGAAATGACGTTGCGCGTATGATATTCGCTATATTTTCCAACTTTATGATTTTGTAG 909  
Db 796 AGAGAAATGACGTTGCGCGTATGATATTTGCTATATTTTCCAACTTTATGATTTTGTAG 855  
QY 910 AAATATCCAATGCGCAACACATGTAGAGTTGACTAGGGAAATTTATACAGATCAGGTGGGA 969  
Db 856 AAATATCCAATTAGCAACAAGTGTAGAGTTAAGTGGGAAATTTATACAGATCAGGTGGGA 915  
QY 970 TATTCATCGGAACTTTATAGTTGGTTACGGAAATTCGCCCTAATATCTTTTAAATGGGTTAGAG 1029  
Db 916 TATTCAGGGGAAATTTATGTTGGGAACGGTTT-----TTAGCTTTAATTTCCGTAGAA 969  
QY 1030 GCTAATGGAACACGCGGACCTGTTTGTAGTTTACTTCTGCTTAGCAAAATAGTATATATAAT 1089  
Db 970 GCAATGGAACACGCGGACCTGTTTGTAGTTTACTTGGCTTCAAGCTATAGATATATATAGT 1029  
QY 1090 GAGTATGTT-----TCGAGATATTTTGGCGCTCGGTAGGAACTCGTCATTTATGAA 1140  
Db 1030 CATTTCTATTAACTTTTTCAGCTTGGTTTATCTTAGTGGCTGGGGGGAACCTGTCATTTAGAA 1089  
QY 1141 GACTACACAAGGGTAAACGGTATTTTTCAAACGATGCTGTGGAACCTACGAGTAATGATCTA 1200  
Db 1090 GACTTCAACAAGGGTAACGGTCTTTTCAACGATGCTGTGGAACCTACGAGTAATGATCTA 1149  
QY 1201 CGTAAATTTGATTTTTCAGATGCGCATGATATAAATTAATTTACTTCTATTTAGCTA---TCATG 1257  
Db 1150 CGTAAATTTATTTTGGCAATACCGATATATTTAAATATTTTCAATTTAGCTAGATATGCA 1209  
QY 1258 AACCTAGTAGGAGAGACTACCGCTAGACAGAGTATCGTGTGTTTCAAGGCGAGATTTTCGT 1317  
Db 1210 ATGCAACCGTTTGTGGGTATTCAATCCACGGCATCTGTTTTCAGTCGAGAAATTTT 1269

```
QY 1318 AGGTAGGGGACCTGATTTAAATTAATGATGAGGTAATAATGGGCTAAGCAGGATGACA 1377
Db 1270 CCGCAACACTAAATACTTCTCTGATGAGGTAACACAGTCTCTGGG---TACTCACAGACA 1326
QY 1378 ATTGAATCTACCTCCACTTCT-----ATTGCACCTCTAATGGTGTAGAGGCCCTCT 1431
Db 1327 ATTGAATCTGTATTACCGGATTAATAAAGGATCTACCACCTAGTCGTACAAATTAATCTCT 1386
QY 1432 CATAGATTAATCAAAATCGCGCATGTGTGTATATGGAACCTCCAGAGTTAAACGTATATGCT 1491
Db 1387 CATAGATTAATCAAAATCGCGCATGTGTCAAAATGAACCTCCAGAGTTAAACGTATTTGCT 1446
QY 1492 TGGACACATCAAGTTTAAACGTGAAATATAAATGAAGCCAAATCAAAATTAACAAATA 1551
Db 1447 TGGACACATCAAGTATGAAAGGATTAATCGAATTTATCCAGATAAAATTAACGCAAT 1506
QY 1552 CCGGCGGTGAAGGTTATTACCTTCAAAATTAATCTTGTCTAATGCCTATACCTATGTAATA 1611
Db 1507 CTGCGAGTAAAGCTTTTGGCCCTACCAGCAGGTACAGSATATGCGAGGAGTTACGTCACA 1566
QY 1612 AAAGGCACT 1620
Db 1567 GCTGGCCT 1575
```

## RESULT 7

```
US-10-099-285-71
; Sequence 71, Application US/10099285
; Publication No. US20030105319A1
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
;            Winkler, Carol
;            Narva, Kenneth E.
;            Walz, Michelle
;            Stockhoff, Brian
;            Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/099,285
; FILING DATE: 15-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,285
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3471 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-099-285-71

Query Match      8.1%; Score 168.6; DB 5; Length 3471;
Best Local Similarity 52.5%; Pred. No. 1e-27;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

QY 156 AATTGGGAATCAGTCGAAACGATAACAAGATTGGGATAAATCTTTATAGAGTTTGTGAT 215
Db 153 AATAGGCCATCGACGAAAAGAGCGATCTATTGGGACAACCATAGTCTCTCTTATCAC 212
QY 216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATPAAATAGGAAATAAT 269
Db 213 AGCACCTTCTTACTCTGATTAATTTCAATAGTATATGACCTTATAGTAAAGTACTAGG 272
QY 270 TCCGACTAATCGTCAAACTGTGTCAGCACTTCTATATGTGATTTTATTTATCTATTAATTCG 329
Db 273 AGGTAGTAGTGGACAAATCCATATCAGATTTGTCTATATGTGACTTATTTATCTATTTTGA 332
QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTGATGCGAATTCAGATTTTGACGGTAAATTTGAA 389
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTTAATGATGGGATTCAGATTTTAAATGGTCTGTACT 392
QY 390 AAATATTAGAGATTAATCTTTCTTATCTTTGGGCTTTGGCTTAAAGACGGTAAACCACT 449
Db 393 CTTATACAGGAACATATTTAGAGGCTCTCGATAGCTGGAATAAGAAATCCTAATTTCTGCTTC 452
QY 450 TCAAAAGACAATAATTCCTGATATCGGACAATTAGTTTATTTATTTTAACTTTTCAAGAAAG 509
Db 453 TGCTGAAGAATCTCGTACTCGTTTTAGAAATCGCCGACTCAGAAATTTGTAGAAATTTTAAAC 512
QY 510 AGATTTTCAATGAAATTTCTAGGAGGTCATTTGTCAGAAACAATGCTCAAGTATTTCTTATT 569
Db 513 CCGAGGCTCTTTACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCATAATTTATTTATT 572
QY 570 ACCTACTTTTGCACAAGCTGCAAAATGTGCAGTTTACTATTAAAGGGATGCAATTTCAATA 629
Db 573 ACCTTCTTTTGGAGCGCTGCATTTTCCATTTTATTTACTACTAAGGGATGCTACTAGATA 632
QY 630 TAAAGCAATAGGTTCCTCCATTTTTCAGTGCAGAGATGTAAGATCGGAATTAATATCACC 689
Db 633 TGGCACTAATTTGGGGGCTATACAAATGCTACACCTTTTATTAATTTATCAATCAAACTAGT 692
QY 690 TAAAGTGTGTGATTTTACCGGTGATTACTATGAGCGATTTAAATATGCAAAACGGCAGA 749
Db 693 AGAGCTTATT-----GAACT 707
QY 750 GTATACCAATTAATGTTTATTTATTTGATTCAGGTAGGTTTAAATCAGATAAAACAGGGGG 809
Db 708 ATATACTGATTATTGCGTACATTTGTAATAATCGAGGTTTCAACGAACTAAGACAAACGAGG 767
QY 810 GACAGTCTGACACTTGGTCGAATTTAAATAATTTGTCAGAGAAATGACGCTGGCCGT 869
Db 768 CACTAGTCTCAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGAGATGACATTTGATGGT 827
QY 870 ATTGGATATTATCGCTATATTTTCCAACTTATGATTTTTCAGAAATATCCATTTGCCAACACA 929
Db 828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTTACCCTAATAGAAACAGA 887
QY 930 TGTAGAGTTGACTAGGGAAATTTATACAGATGTCAGTGGGATTTATCATCGGGAACTTTATAG 989
Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATTTGTTTGTACATCGTAGTAGTCT 947
QY 990 TTGTTTACGGAATTTGGCCTTAATCTTTTAAATCG 1022
Db 948 TAGGGGAGAAAGTTGGTTTAGCTTTTGTAAATAG 980

RESULT 8
US-10-428-961-29
```

; Sequence 29, Application US/10428961  
; Publication No. US20030237111A1  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Ruper, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin  
; TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)  
; FILE REFERENCE: MCO201-1  
; CURRENT APPLICATION NUMBER: US/10/428,961  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/661,322  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: 60/153,995  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 2407  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-10-428-961-29

Query Match 7.7%; Score 160.6; DB 6; Length 2407;  
Best Local Similarity 51.9%; Pred. No. 5.7e-26;  
Matches 453; Conservative 0; Mismatches 369; Indels 51; Gaps 2;  
QY 156 AATTGGGAATCAGTCGAAACGATAACAGATATGGGATAAATCTTATAGAGTTTGTGAT 215  
Db |||||  
QY 153 AATAGGCGATGCGACAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTATCAC 212  
Db |||||  
QY 216 AGAACCTAGTTGGGTGGATTAATACACTATTAT-----CAATAATAGGAAAACCTAAT 269  
Db |||||  
QY 213 AGCACCTTCTCTACTGGATTAATTTCAATAGTATATAGACCTTATATAGTAAGTACTAGG 272  
Db |||||  
QY 270 TCCGACTAATCGTCAAACTGTGTCAGCACCTTCTATATGTGATTTATATCTATAATTCG 329  
Db |||||  
QY 273 AGGTAGTAGGACATCCATATCAGATTTGTCTATATGTGACTTATATCTATATTGA 332  
Db |||||  
QY 330 TAAAGAGTAGCGAGTAGTGTTTTAAAGTATGCGATGCGATTTTGCAGCGTAAATTTGAA 389  
Db |||||  
QY 333 TTTACGGTAAAGTCAGAGTGTTTTAAATGATGGATTGCGAGATTTTAAATGTTCTGTACT 392  
Db |||||  
QY 390 AAATTATAGAGATATATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 449  
Db |||||  
QY 393 CTTATACAGGAATATTTAGAGGCTCTGGATAGCTGGAATPAAGAACTCTAATTTCTGCTTC 452  
Db |||||  
QY 450 TCAAAAGACAAATAATTTCTGATATCGACAATTTAGTTTATTTTAAACTTTTCAGAAAG 509  
Db |||||  
QY 453 TGTGGAAGAACTCGGTACTCTGTTTAAATCGCGACTCAGATTTGTATAGAAATTTTAAAC 512  
Db |||||  
QY 510 AGATTTCAATGAAATCTTAGGAGGGTCATTTGCAAGAAACAATGCTCAAGATATTGTATT 569  
Db |||||  
QY 513 CCGAGGCTCTTAAACGAATGGTGGCTCGTTAGCTAGACAAAATGCCCAAATATTTATT 572  
Db |||||  
QY 570 ACCTACTTTTGCACAGCTGCAATGTGCGATTTTACTATTTAAGGATGCGAGTTCAATA 629  
Db |||||  
QY 573 ACCTCTTTTGGAGCGCTGCATTTTTCATTTTACTACTAAGGGATGCTACTAGATA 632  
Db |||||  
QY 630 TAAAGCACAAATGCTCCATTTTGTAGTCAGAGAATGTAAGATCGGAATTAATAATCAACC 689  
Db |||||  
QY 633 TGCACATTAATTTGGGGCTATACAACTGCTACACCTTTTAAATTTATCAATCAAACTAGT 692  
Db |||||  
QY 690 TAAAGTGGTGTGATTTTACCGGTGATTTACTATAGCGGATTAATAATGCAAAACGGCAGA 749  
Db |||||  
QY 693 AGAGCTATT-----GAACT 707  
Db |||||  
QY 750 GTATACCAATTTATTTTATTTTATTTGGTATCAGGTAGGTTTAAATCAGATAAACAGGGGG 809  
Db |||||  
QY 708 ATATACTGATTTATTTGGTATCATTGGGATTAATCGAGGTTCAACCGGAACCTAAGCAACGAG 767  
Db |||||

## RESULT 9

US-10-120-544A-19  
; Sequence 19, Application US/10120544A  
; Publication No. US20020192693A1  
; GENERAL INFORMATION:  
; APPLICANT: TANAKA, Masao  
; APPLICANT: YOKOYAMA, Tomoko  
; APPLICANT: AOYAGI, Moriichi  
; APPLICANT: HASEGAWA, Makoto  
; APPLICANT: EHARA, Gaku  
; APPLICANT: KIMURA, Masaharu  
; APPLICANT: NISHIHASHI, Hideji  
; TITLE OF INVENTION: Polyptide having larvae growth inhibiting or  
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
; TITLE OF INVENTION: polynucleotide encoding the same  
; FILE REFERENCE: OP1335  
; CURRENT APPLICATION NUMBER: US/10/120,544A  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: JP 2001-115754  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: JP 2001-203463  
; PRIOR FILING DATE: 2001-07-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 4366  
; TYPE: DNA  
; ORGANISM: Bacillus popilliae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (224)..(4255)  
US-10-120-544A-19  
Query Match 4.9%; Score 102.4; DB 5; Length 4366;  
Best Local Similarity 58.0%; Pred. No. 1.5e-12;  
Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;  
QY 716 ATTACTATCAGCGATTAAATGCAAAACGCGAGAGTATACCAATTTATTTTATATTGGT 775  
Db |||||  
QY 921 ATATTTACAATGCCACAAAGAACTCCGCAACGTATGCAATCATTTGTACAACTTGGT 980  
Db |||||  
QY 776 ATCAGGTAGTTTAAATCAGATATAAAGACGGGGGAGCAGGTGCTGACACTTGGTCGAAT 835  
Db |||||  
QY 981 ATCAGACGGGTTTACA-----AAGATTCAAGGCGAGCGATGCTAGCAGTTGGTCAA 1034  
Db |||||  
QY 836 TTAATAAATTTTGTAGAGAAATGACGTTGGCGGTATTTGATATTTATTCCTATATTCCAA 895  
Db |||||  
QY 1035 ATAAATCGATTTAGAGAGAAATAACGTTAATAGTATTTGATTTTGTGCAATTTGTTTCAA 1094  
Db |||||  
QY 896 CTTATGATTTTGTAGAAATCCATTTGCCAAACACATGTAGAGTTGACTAGGAAATTTATA 955  
Db |||||  
QY 1095 ATTATGATGTTTGTAGTTATCCAAATACAGTTACGGGGAGAGCTTACAGAGGAATTTATA 1154  
Db |||||  
QY 956 CAGATCGAGTGGGATATTTCATCGGGAATTTATAGTTGGTTACGGAATTTGGCCTTAATCTT 1015  
Db |||||  
QY 1155 CGGATCCAGCAGTATATACGGGTACAGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1214  
Db |||||



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; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3687)
US-10-428-961-37

Query Match      4.6%; Score 95.6; DB 6; Length 4173;
Best Local Similarity 62.7%; Pred. No. 5.3e-11;
Matches 168; Conservative 0; Mismatches 94; Indels 6; Gaps 1;

QY 717 TTACTATGAGGATTAAATGCAAAACGGCAGAGTATACCAATATTGTTTATTTGGTA 776
Db 645 TTATTATGAGCGCAAGTGGAAACAACGAGAGATTATTCGCAATTATTCGATAGAGTGA 704
QY 777 TCAGGTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTCGTGACACTTGGTCGAAAT 836
Db 705 TAATACAGGTCTAAATAGCTTGAGA-----GGGCAAAATGCCGCAAGTTGGGTGCGTTA 758
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGGGGTATTGGATATTATCGCTATATTTCCAAC 896
Db 759 TAATCAATTCGTTAGAGATCTAAGTTAGGGGTATTAGATCTAGTGCACATATTCOAAG 818
QY 897 TTATGATTTTGAGAAATATCCATTGGCAACACATGTAGAGTTGACTAGGGAAATTTATAC 956
Db 819 CTATGACACTCGCACTTATCCAAATAATACGAGTGCTCAGTTAAACAAGGGAAGTTTATAC 878
QY 957 AGATGCACTGGGATATTCATCGGNACT 984
Db 879 AGACGCAATTTGGAGCAACAGGGGTAAAT 906

RESULT 13
US-10-544A-3
; Sequence 3, Application US/10120544A
; Publication No. US20020182693A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/10/120,544A
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-10-120-544A-3

Query Match      4.6%; Score 95.2; DB 5; Length 4359;
Best Local Similarity 62.0%; Pred. No. 6.7e-11;
Matches 170; Conservative 0; Mismatches 98; Indels 6; Gaps 1;

QY 696 TGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACCGCAGAGTATAC 755
Db 1025 TGCTCAAGCTACTATTGACAATAATTACATGCCAAATAAGAAACCGCAGAGTATGC 1084
QY 756 CAATTATTGTTTATATTGGTATCAGGTAGGTTTAAATCAGATAAACAAGGGGGGACAGG 815
Db 1085 AAATCATTTGTACCACCTTGGTATCAGACGGGTTTACA-----AAGATTGCAAGGCACTAC 1138
QY 816 TGCTGACACTTGGTCGAAATTTAAATAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGA 875
Db 1139 TGCTAGCAGTTGGCTCTCTTATCATAGATTAGAGAGAGAAATGACACTAACAGTATTGGA 1198
QY 876 TATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGA 935
Db 1199 TATTTCGCAATTTATTTTCAATTTATGATGCCCGTAGTTACCCACTGGAGGTAAAGGGGAGA 1258
QY 936 GTTGACTAGGGAAATTTATACAGATGCAGTGGGA 969
Db 1259 GCTTACGAGAGAAATTTATACGGATCCAGTAGCA 1292

RESULT 14
US-11-091-654-3
; Sequence 3, Application US/11091654
; Publication No. US20050172355A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Morichi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: poynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,654
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-654-3

Query Match      4.6%; Score 95.2; DB 10; Length 4359;
Best Local Similarity 62.0%; Pred. No. 6.7e-11;
Matches 170; Conservative 0; Mismatches 98; Indels 6; Gaps 1;

QY 696 TGGTTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACCGCAGAGTATAC 755
Db 1025 TGCTCAAGCTACTATTGACAATAATTACATGCCAAATAAGAAACCGCAGAGTATGC 1084
QY 756 CAATTATTGTTTATATTGGTATCAGGTAGGTTTAAATCAGATAAACAAGGGGGGACAGG 815
Db 1085 AAATCATTTGTACCACCTTGGTATCAGACGGGTTTACA-----AAGATTGCAAGGCACTAC 1138
QY 816 TGCTGACACTTGGTCGAAATTTAAATAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGA 875
Db 1139 TGCTAGCAGTTGGCTCTCTTATCATAGATTAGAGAGAGAAATGACACTAACAGTATTGGA 1198
QY 876 TATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGA 935
Db 1199 TATTTCGCAATTTATTTTCAATTTATGATGCCCGTAGTTACCCACTGGAGGTAAAGGGGAGA 1258
QY 936 GTTGACTAGGGAAATTTATACAGATGCAGTGGGA 969
Db 1259 GCTTACGAGAGAAATTTATACGGATCCAGTAGCA 1292
```

```
RESULT 15
US-10-428-961-5
; Sequence 5, Application US/10428961
; Publication No. US20030237111A1
; GENERAL INFORMATION:
; APPLICANT: Baum, James A.
; APPLICANT: Chu, Chih-Rei
; APPLICANT: Donovan, William P.
; APPLICANT: Gilmer, Amy J.
; APPLICANT: Rupar, Mark J.
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
; FILE REFERENCE: Polynucleotides, Compositions, and Methods of Use (Amended)
; CURRENT APPLICATION NUMBER: US/10/428,961
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/661,322
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 60/153,995
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-10-428-961-5

Query Match      4.5%; Score 94.4; DB 6; Length 1959;
Best Local Similarity 62.2%; Pred. No. 7.1e-11;
Matches 168; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY      716 ATTACTATGAGCGATTAAAAATGCAAAACGCGAGAGTATACCAATTATTGTTTATATTGGT 775
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      629 AATATTACCGAGNACAAATCAGATATACAGAGGAATATTCTAACCATTCGGTACATGGT 688
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      776 ATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGGACAGGTGCTGACACTTGGTCGAAAT 835
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      689 ATAATACAGGGCTAAATAACTTAA-----GAGGGACAAATGCTGAAAGTTGGTTGCGGT 742
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      836 TTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCCAA 895
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      743 ATAATCAATTCGTAAGACCTTAACGTTAGGGGTATTAGATTATTAGTGGCCCTATTCCCAA 802
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      896 CTTATGATTTTGAGAAATATCCATTGCCAACACATGATAGATTGACTAGGGAAATTTATA 955
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      803 GCTATGATCTCGCACTTATCCAAATCAATACGAGTGCTCAGTTAACAGAGAAATTTATA 862
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      956 CAGATCGAGTGGGATATTTCATCGGGAACCTT 985
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      863 CAGATCCAATTGGGAGAACAAATGCACCTT 892
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Job time : 1035.64 secs



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OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 14:38:00 ; Search time 135.839 Seconds  
(without alignments)  
7512.972 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4161431 seqs, 245089505 residues

Total number of hits satisfying chosen parameters: 8322862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description      |
|------------|-------|-------------|--------|-------|------------------|
| 1          | 102.4 | 4.9         | 4366   | 9     | US-11-091-643-19 |
| 2          | 99.2  | 4.8         | 4119   | 7     | US-11-070-575-4  |
| 3          | 95.2  | 4.6         | 4359   | 9     | US-11-091-643-3  |
| 4          | 91.4  | 4.4         | 4188   | 9     | US-11-091-643-5  |
| 5          | 87.8  | 4.2         | 1860   | 7     | US-11-058-727-15 |
| 6          | 87.8  | 4.2         | 1860   | 7     | US-11-058-389-15 |
| 7          | 87.8  | 4.2         | 1863   | 7     | US-11-058-727-19 |
| 8          | 87.8  | 4.2         | 1863   | 7     | US-11-058-389-19 |
| 9          | 87.8  | 4.2         | 2010   | 7     | US-11-058-727-11 |
| 10         | 87.8  | 4.2         | 2010   | 7     | US-11-058-389-11 |
| 11         | 87.8  | 4.2         | 2019   | 7     | US-11-058-727-57 |
| 12         | 87.8  | 4.2         | 2019   | 7     | US-11-058-727-59 |
| 13         | 87.8  | 4.2         | 2019   | 7     | US-11-058-727-89 |
| 14         | 87.8  | 4.2         | 2019   | 7     | US-11-058-727-91 |
| 15         | 87.8  | 4.2         | 2019   | 7     | US-11-058-389-57 |
| 16         | 87.8  | 4.2         | 2019   | 7     | US-11-058-389-59 |
| 17         | 87.8  | 4.2         | 2019   | 7     | US-11-058-389-89 |
| 18         | 87.8  | 4.2         | 2019   | 7     | US-11-058-389-91 |
| 19         | 87.8  | 4.2         | 2022   | 7     | US-11-058-727-7  |
| 20         | 87.8  | 4.2         | 2022   | 7     | US-11-058-727-21 |
| 21         | 87.8  | 4.2         | 2022   | 7     | US-11-058-727-25 |
| 22         | 87.8  | 4.2         | 2022   | 7     | US-11-058-727-29 |
| 23         | 87.8  | 4.2         | 2022   | 7     | US-11-058-727-33 |

ALIGNMENTS

RESULT 1

US-11-091-643-19

; Sequence 19, Application US/11091643

; Publication No. US20050246789A1

; GENERAL INFORMATION:

; APPLICANT: TANAKA, Masao

; APPLICANT: YOKOYAMA, Tomoko

; APPLICANT: AOYAGI, Moriichi

; APPLICANT: HASEGAWA, Makoto

; APPLICANT: EHARA, Gaku

; APPLICANT: KIMURA, Masaharu

; APPLICANT: NISHIHASHI, Hideji

; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or

; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and

; FILE REFERENCE: OPI335

; CURRENT APPLICATION NUMBER: US/11/091,643

; PRIOR FILING DATE: 2005-03-29

; PRIOR APPLICATION NUMBER: JP 2001-115754

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: JP 2001-203463

; PRIOR FILING DATE: 2001-07-04

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 4366

; TYPE: DNA

; ORGANISM: Bacillus popilliae

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (224)..(4255)

US-11-091-643-19

Query Match

Best Local Similarity 4.9%; Score 102.4; DB 9; Length 4366;

Matches 203; Conservative 0; Mismatches 141; Indels 6; Gaps 1;

|    |     |  |      |
|----|-----|--|------|
| QY | 716 | ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATTTGGT   | 775  |
| DB | 921 | ATAATTACAATCGCAACAAAGAACTCGCAACGTATGCAATCATTTGTACAACTTGGT    | 980  |
| QY | 776 | ATCAGGTAGTTTAATTCAGATAAAACAGGGGGGACAGGTCTGACACTTGGTCAAAAT    | 835  |
| DB | 981 | ATCAGACGGGTTTAC-----AAGATTGCAAGGCGAGCATGCTAGCAGTTGGTCAAAAT   | 1034 |
| QY | 836 | TTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGTATATTTCCAA | 895  |

```
Db      1035  ATAAATCGATTGAGAGAAATAACGTTAATAGTATTGGATATTTGTCATTGTTTTCAA 1094
QY      896  CTTATGATTGTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGCGAAATTTATA 955
Db      1095  ATTATGATGTTGCTAGTTATCCATACAGTTACGGGAGAGCTTACGAGAGNAATTTATA 1154
QY      956  CAGATCAGTGGGATATTCATCGGGAACCTATATAGTTGGTTGCGGAATGCGCCCTAATPACTT 1015
Db      1155  CGGATCCAGCAGTATATAGCGGTACAGGTTCCCTATTCTGTTGAGTCAAGCACCATCAT 1214
QY      1016  TTAATCGGTAGAGGCTAATGNAACACGGGACCTGTTTAGTTACTTGG 1065
Db      1215  TTGCAGAAATAGAAATATCGCAATTTAGGNAACCAAGCAATTTTACTTGG 1264
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## RESULT 2

```
US-11-070-575-4
; Sequence 4, Application US/11070575
; Publication No. US20050271642A1
; GENERAL INFORMATION:
; APPLICANT: ASANO, Shin-ichiro
; APPLICANT: NOZAWA, Mikiko
; APPLICANT: BANDO, Hisanori
; TITLE OF INVENTION: RECOMBINANT ORGANISMS PRODUCING INSECT
; TITLE OF INVENTION: TOXINS AND METHODS FOR CONSTRUCTING SAME
; FILE REFERENCE: 59562200300
; CURRENT APPLICATION NUMBER: US/11/070,575
; PRIOR FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: US 60/549,094
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4119
; TYPE: DNA
; ORGANISM: Bacillus popilliae
US-11-070-575-4
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Query Match      4.8%; Score 99.2; DB 7; Length 4119;
Best Local Similarity 57.4%; Pred. No. 1.4e-13;
Matches 201; Conservative 0; Mismatches 143; Indels 6; Gaps 1;

QY      716  ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATGTTTATATGTT 775
Db      768  ATAATTACAATCGCCAAACAAAGAACTCGGCAACGTATGCAATTCAATTGTACAACTTGGT 827
QY      776  ATCAGTAGTGTTAATCAGATAAAACAGGGGGACAGGTGCTGACACTTGTTCGAAT 835
Db      828  ATCAGACGGGTTTACA-----AAGATTGCAAGGCAGCATGCTAGCAGTTGGGTCAATT 881
QY      836  TTAATAAAATTCGTAGAGAAATGACGTTGCGGTATTTGGATATTTATCGCTATATTTCCAA 895
Db      882  ATAATCGATTGAGAGAAATAACGTTAATAGTATTGGATTTGTCATTGTTTTCAA 941
QY      896  CTTATGATTGTGAGAAATATCCATTCGCAACACATGTAGAGTTGACTAGCGAAATTTATA 955
Db      942  ATTATGATGTTGCTAGTTATCCAATACAGTTACGGGGAGAGCTTACGAGAGGAATTTATA 1001
QY      956  CAGATCAGTGGGATATTCATCGGGAACCTATAGTTGGTTACGGAATGCGCCTAATACCT 1015
Db      1002  CGGATCCAGCAGTATTTAGCGGTACAGGTTCCCTATTCTGTTGAGTCAAGCACCATCAT 1061
QY      1016  TTAATGGGTTAGAGGCTAATGGAACACAGGGGACCTCGTTTAGTTACTTGG 1065
Db      1062  TTGCAGAAATAGAAATATCGCAATTTAGGNAACCAAGCAATTTTACTTGG 1111
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## RESULT 3

```
US-11-091-643-3
; Sequence 3, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
```

```
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4359
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (282)..(4229)
US-11-091-643-3
```

```
Query Match      4.6%; Score 95.2; DB 9; Length 4359;
Best Local Similarity 62.0%; Pred. No. 1.2e-12;
Matches 170; Conservative 0; Mismatches 98; Indels 6; Gaps 1;

QY      696  TGGTTGTGATTTTACC GGTTACTATGAGCGATTAAATGCAAAACGGCAGAGTATAC 755
Db      1025  TGCTCAAGCTACTATTGACAATAATTACAATCGCCAAATAAGGAAACCGCAGAGTATGC 1084
QY      756  CAATTATTGTTTATGTTATCGTATCAGTAGGTTTAAATCAGATAAAACAGGGGGGACAGG 815
Db      1085  AAATCATTTGTACCACTTGTGTATCAGACGGGTTTACA-----AAGATTGCAAGGCACCTAC 1138
QY      816  TGCTGACACTTGGTGGAAATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGA 875
Db      1139  TGCTAGCAGTTGGCTCTCTTATCATAGATTTAGAAAGAAATGACACTAACAGTATTGGA 1198
QY      876  TATTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGA 935
Db      1199  TATTTGGCGATTATTTTCAAAATTATGATGCCGTAGTTACCCACTGGAGGTAAGGGGAGA 1258
QY      936  GTTGACTAGGGAATTTTATACAGATGTCAGTGGGA 969
Db      1259  GCTTACGAGAGAAATTTTATACGGATCCAGTAGCA 1292
```

## RESULT 4

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US-11-091-643-5
; Sequence 5, Application US/11091643
; Publication No. US20050246789A1
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Masao
; APPLICANT: YOKOYAMA, Tomoko
; APPLICANT: AOYAGI, Moriochi
; APPLICANT: HASEGAWA, Makoto
; APPLICANT: EHARA, Gaku
; APPLICANT: KIMURA, Masaharu
; APPLICANT: NISHIHASHI, Hideji
; TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or
; TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and
; TITLE OF INVENTION: polynucleotide encoding the same
; FILE REFERENCE: OPI335
; CURRENT APPLICATION NUMBER: US/11/091,643
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: JP 2001-115754
; PRIOR FILING DATE: 2001-04-13
```

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; PRIOR APPLICATION NUMBER: JP 2001-203463
; PRIOR FILING DATE: 2001-07-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4188
; TYPE: DNA
; ORGANISM: Bacillus popilliae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4158)
US-11-091-643-5

Query Match          4.4%; Score 91.4; DB 9; Length 4188;
Best Local Similarity 61.1%; Pred. No. 8.7e-12;
Matches 168; Conservative 0; Mismatches 101; Indels 6; Gaps 1;

QY 715 GATTACTATGAGCGATTAAATCAAACGGCAGAGTATACCAATTATTGTTTATATG 774
Db 766 GATAATTATAATCTCAATAAGCGCTCTGCAGATTATGCAATCATTTGTACAACCTGG 825
QY 775 TATCAGTAGGTTTAAATCAGATAAACAAGGGGGGACAGGCTGCACACTTGGTCGAAA 834
Db 826 TATCGGACGGGTTTACA-----AGATTGCAAGGCCCAATGCTAGCAGTTGGGTCAAT 879
QY 835 TTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTCCA 894
Db 880 TATAATCGATTATAGAGAGAAATGACACTAATGTTATTAGATGTTTGTGCATTTATTTCA 939
QY 895 ACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTAT 954
Db 940 AGTTATGATTATCGTAGTTTACCCAATGGAGCTAAGGGGAGAGCTTACGAGAGAAATTTAT 999
QY 955 ACAGATGCACTGGGATTAATCAATCGGAACCTTAG 989
Db 1000 ACGATCCAGTAGGACGCTCTTTTGGGTGAATAG 1034
```

```
RESULT 5
US-11-058-727-15
; Sequence 15, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) ... (1860)
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: 49PVD
US-11-058-727-15

Query Match          4.2%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATG 773
Db 555 TAACTATTATGATCGTCAAACTTACTCGAGAATATTCTGATCACTGTGTAAAGTG 614
QY 774 GTATCAGTAGGTTTAAATCAGATAAACAAGGGGGGACAGGTCGTGACACTTGGTCGAA 833
Db 615 GTATGAACCTGGTTTAGCAAAATTTAAA-----GGCACGAGCGCTAAACAATTTGA 668
QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTC 893
Db 669 CTATAACCAATTCGTTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTATTCCC 728
QY 894 ACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 729 AAATTATGACACACGCGTACCAATGGAACGAAAGCAACAATAACAAGGGAAGTATA 788
QY 954 TACAGATGAGGCGGATATTCATCGGAACCTTATAGTTGGTTACGGAAT 1002
Db 789 TACAGATCCACTGGGCGGTAAACGCTGCTTCAATTGTTCTCTGCTAT 837
```

```
RESULT 6
US-11-108-389-15
; Sequence 15, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F. H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE OF INVENTION: Activity
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1860
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (truncated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10) ... (1860)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0) ... (0)
; OTHER INFORMATION: 49PVD
US-11-108-389-15
```

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Query Match          4.2%; Score 87.8; DB 7; Length 1860;
Best Local Similarity 59.2%; Pred. No. 4.4e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;
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QY 714 TGATTAATAATTCGTAGAGAAATGCAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773  
Db 555 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATCTGATCACTGTGTAAAGTG 614  
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGTGACACTTGGTCGAA 833  
Db 615 GTATGAAACTGGTTTACGAAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 668  
QY 834 ATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATCGCTATATTTCC 893  
Db 669 CTATTAACCAATTCGCTAGAGAAATGACACTGGCGGTTTGTAGATGTTGTGCATTAATTTCC 728  
QY 894 AACTTATGATTTTGAGAAATTCCTATGCAACACATGTAGAGTTGACTAGGGAATTTA 953  
Db 729 AAATTATGACACAGCGACGTCACCAATGGAACGAAAGCACAACTAAACAAGGGAAGTATA 788  
QY 954 TACAGATGACGAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAAT 1002  
Db 789 TACAGATCCACTGGCGCGGTAAACGTTGCTTCAATTTGGTTCCTGGTAT 837

## RESULT 7

US-11-058-727-19  
; Sequence 19, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 1863  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1863)  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: NGRS.N49PVD  
US-11-058-727-19

Query Match 4.2%; Score 87.8; DB 7; Length 1863;  
Best Local Similarity 59.2%; Pred. No. 4.4e-11;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;  
QY 714 TGATTAATAATTCGTAGAGAAATGCAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773  
Db 558 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATCTGATCACTGTGTAAAGTG 617  
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGTGACACTTGGTCGAA 833  
Db 618 GTATGAAACTGGTTTACGAAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 671

QY 834 ATTTAATAAATTCGTAGAGAAATGCAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 893  
Db 672 CTATTAACCAATTCGTAGAGAAATGACACTGGCGGTTTGTAGATGTTGTGCATTAATTTCC 731  
QY 894 AACTTATGATTTTGAGAAATTCCTATGCAACACATGTAGAGTTGACTAGGGAATTTA 953  
Db 732 AAATTATGACACACGACGTCACCAATGGAACGAAAGCACAACTAAACAAGGGAAGTATA 791  
QY 954 TACAGATGACGAGTGGGATATTCATCGGGAACCTTATAGTTGGTTACGGAAT 1002  
Db 792 TACAGATCCACTGGCGCGGTAAACGTTGCTTCAATTTGGTTCCTGGTAT 840

## RESULT 8

US-11-108-389-19  
; Sequence 19, Application US/11108389  
; Publication No. US20050261188A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; FILE OF INVENTION: Activity  
; FILE REFERENCE: 35718/291049  
; CURRENT APPLICATION NUMBER: US/11/108,389  
; PRIOR FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; PRIOR FILING DATE: 2003-06-25  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 1863  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1863)  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: NGRS.N49PVD  
US-11-108-389-19

Query Match 4.2%; Score 87.8; DB 7; Length 1863;  
Best Local Similarity 59.2%; Pred. No. 4.4e-11;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;  
QY 714 TGATTAATAATTCGTAGAGAAATGCAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 773  
Db 558 TAACTATTATGATCGTCAAAATGAAACTTACTGAGAAATATCTGATCACTGTGTAAAGTG 617  
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGAGAGTGTGACACTTGGTCGAA 833  
Db 618 GTATGAAACTGGTTTACGAAAAATTAATA-----GGCAGAGCGCTTAAACAATGGGTTGA 671  
QY 834 ATTTAATAAATTCGTAGAGAAATGCAAAATGCAAAACGGCAGAGTATACCAATATTGTTTATATG 893  
Db 672 CTATTAACCAATTCGCTAGAGAAATGACACTGGCGGTTTGTAGATGTTGTGCATTAATTTCC 731  
QY 894 AACTTATGATTTTGAGAAATTCCTATGCAACACATGTAGAGTTGACTAGGGAATTTA 953  
Db 732 AAATTATGACACACGACGTCACCAATGGAACGAAAGCACAACTAAACAAGGGAAGTATA 791

Qy · 954 TACAGATGCAGTGGGATATTTCATCGGAACTTATAGTTGTTACGGAAT 1002  
|||  
Db 792 TACAGATCCACTGGGGCGGTAACGTGCTTCAATTGGTTCCTGGTAT 840  
|||

RESULT 9  
US-11-058-727-11  
; Sequence 11, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Presnail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu

```

APPLICANT: CRO-GUC RU
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2010
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-058-727-11

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| Query Match           | 4.2%; Score 87.8; DB 7; Length 2010;                                    |
|-----------------------|---|
| Best Local Similarity | 59.2%; Pred. No. 4.5e-11;   |
| Matches               | 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;                  |
| Qy                    | 714 TGATTACTATGAGCGATTAAATCCAAACGGCAGAGATATACCAATTATTGTTTATATTG 773     |
| Db                    | 687 TAACTATTATGATCGTCAAAATGAAACCTACTGCGAATATTTCTGATCACTGTGTAAGTG 746    |
| Qy                    | 774 GTATCAGGTAGTGTTTAAATCAGATATAAACAGCGGGGACAGCGTCTGCACACTTCGTGCA 833   |
| Db                    | 747 GTTATGAACCTGGTTTACGAATAATTAATA-----GGCACGAGCGCTAAACAATGGTGTGA 800   |
| Qy                    | 834 ATTTAATAAAATTTTCGTAGAGAAATGACGTTGGCGGTATTGGATATTATTCGTATTATTTCC 893 |
| Db                    | 801 CTATNACCAATTCGTAGAGNAATGACACTGGCGGTTTATAGATTGTTGCAATTATTTCCC 860    |
| Qy                    | 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGCGGAATTTTA 953   |
| Db                    | 861 AAATTATGACACACGACGCTACCCAAATGGRAAACGAAAGCAACACTAACAGGGAAGTATA 920   |
| Qy                    | 954 TACAGATGCAGTGGGATATTTCATCGGGAACTTATAGTTGGTTACGGAAAT 1002            |
| Db                    | 921 TACAGATTCCTAGTGGCGGGTAAACGCTGTCTTTCAATTGGTTCTCTGGTAT 969            |

RESULT 10  
US-11-108-389-11

```
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-57

Query Match      4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTTGTTATTTG 773
Db 699 TAACTATTATGATCGTCAAACTTACTGCGAATATTTCTGATCACTGTGTAAGTG 758
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGTGTGACACTTTGGTCGAA 833
Db 759 GTATGAACTGTTTAGCAAAATTAAAA-----GGCAGAGCGCTAAACAATGGTTGA 812
QY 834 ATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCC 893
Db 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTATTTCC 872
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 873 AAATTATGACACACGTACGTAACCAATGGAACGAAAGCACAACTAACAGGGAAGTATA 932
QY 954 TACAGATGCGGTGGATATTTCATCGGGAACTTATAGTTGTTTACGGAAT 1002
Db 933 TACAGATCCACTGGGCGGTAACGTCGTCCTTCAATTGGTTCTCGGTAT 981

RESULT 12
US-11-058-727-59
; Sequence 59, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)

; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
US-11-058-727-59

Query Match      4.2%; Score 87.8; DB 7; Length 2019;
Best Local Similarity 59.2%; Pred. No. 4.5e-11;
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTTGTTATTTG 773
Db 699 TAACTATTATGATCGTCAAACTTACTGCGAATATTTCTGATCACTGTGTAAGTG 758
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGTGTGACACTTTGGTCGAA 833
Db 759 GTATGAACTGTTTAGCAAAATTAAAA-----GGCAGAGCGCTAAACAATGGTTGA 812
QY 834 ATTTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTTGGATATTTATCGCTATATTTCC 893
Db 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTAGATGTTGTCATTATTTCC 872
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAATTTA 953
Db 873 AAATTATGACACACGTACGTAACCAATGGAACGAAAGCACAACTAACAGGGAAGTATA 932
QY 954 TACAGATGCGGTGGATATTTCATCGGGAACTTATAGTTGTTTACGGAAT 1002
Db 933 TACAGATCCACTGGGCGGTAACGTCGTCCTTCAATTGGTTCTCGGTAT 981

RESULT 13
US-11-058-727-89
; Sequence 89, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis (mutated)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2019)
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US-11-058-727-89

Query Match 4.2%; Score 87.8; DB 7; Length 2019;  
Best Local Similarity 59.2%; Pred. No. 4.5e-11;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTTATTTTATATTG 773  
DB 699 TAACTATTATGATCGTCAATGAAACTTACTGCGAATATTTCTGATCACTGTGTAAAGTG 758  
QY 774 GTATCAGTGGTTTAAATCAGATAAAACAGGGGGGACAGTGCTGACACTTGGTCGAA 833  
DB 759 GTATGAACACTGGTTTAGCAAAATTAATA-----GGCAGCAGCGCTAAACAATGGGTGA 812  
QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATATTTATCGTATATTC 893  
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTTCCC 872  
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953  
DB 873 AAATTATGACACACTGACGTACCAATGGAACGAAAGCACAACCTAACAGGGAAGTATA 932  
QY 954 TACAGATGCAGTGGGATATTCATCGGAACTTATAGTTGGTTACGGAAT 1002  
DB 933 TACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTGGTTCTCTGGTAT 981

RESULT 14

US-11-058-727-91  
; Sequence 91, Application US/11058727  
; Publication No. US20050261483A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Prenail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/287809  
; CURRENT APPLICATION NUMBER: US/11/058,727  
; PRIOR FILING DATE: 2005-02-15  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)... (2019)  
US-11-058-727-91

Query Match 4.2%; Score 87.8; DB 7; Length 2019;  
Best Local Similarity 59.2%; Pred. No. 4.5e-11;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTTATTTATATTG 773  
DB 699 TAACTATTATGATCGTCAATGAAACTTACTGCGAATATTTCTGATCACTGTGTAAAGTG 758  
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAA 833

DB 759 GTATGAACACTGGTTTAGCAAAATTAATA-----GGCAGCAGCGCTAAACAATGGGTGA 812  
QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATATTTATTCCTATATTTCC 893  
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTTCCC 872  
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953  
DB 873 AAATTATGACACAAATGACGTACCAATGGAACGAAAGCACAACCTAACAGGGAAGTATA 932  
QY 954 TACAGATGCAGTGGGATATTCATCGGAACTTATAGTTGGTTACGGAAT 1002  
DB 933 TACAGATCCACTGGCGCGGTAAACGCTGCTTCAATTGGTTCTCTGGTAT 981

RESULT 15

US-11-108-389-57  
; Sequence 57, Application US/11108389  
; Publication No. US20050261188A1  
; GENERAL INFORMATION:  
; APPLICANT: Andre R. Abad  
; APPLICANT: Ronald D. Flannagan  
; APPLICANT: Rafael Herrmann  
; APPLICANT: Theodore W. Kahn  
; APPLICANT: Albert L. Lu  
; APPLICANT: Billy Fred McCutchen  
; APPLICANT: James K. Prenail  
; APPLICANT: James F.H. Wong  
; APPLICANT: Cao-Guo Yu  
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: 35718/291049  
; CURRENT APPLICATION NUMBER: US/11/108,389  
; PRIOR FILING DATE: 2005-04-18  
; PRIOR APPLICATION NUMBER: 60/391,786  
; PRIOR FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: 60/460,787  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 10/606,320  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 2019  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis (mutated)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)... (2019)  
US-11-108-389-57

Query Match 4.2%; Score 87.8; DB 7; Length 2019;  
Best Local Similarity 59.2%; Pred. No. 4.5e-11;  
Matches 171; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

QY 714 TGATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTTATTTATATTG 773  
DB 699 TAACTATTATGATCGTCAATGAAACTTACTGCGAATATTTCTGATCACTGTGTAAAGTG 758  
QY 774 GTATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAA 833  
DB 759 GTATGAACACTGGTTTAGCAAAATTAATA-----GGCAGCAGCGCTAAACAATGGGTGA 812  
QY 834 ATTTAATAAATTTTCGTAGAGAAATGACGTTGGCGGTATTTGATATTTATTCCTATATTTCC 893  
DB 813 CTATAACCAATTCGTAGAGAAATGACACTGGCGGTTTATAGATGTTGTCATATTTCCC 872  
QY 894 AACTTATGATTTTGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGGAAATTTA 953  
DB 873 AAATTATGACACACGCTAGTACCAATGGAACGAAAGCACAACCTAACAGGGAAGTATA 932  
QY 954 TACAGATGCAGTGGGATATTCATCGGAACTTATAGTTGGTTACGGAAT 1002

Db 933 TACAGATCCACTGGGCGGTAAACGTGTCTTCAATTGGTTCTCTGGTAT 981

Search completed: December 20, 2005, 04:58:17  
Job time : 137.839 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2005, 13:41:30 ; Search time 237.847 Seconds  
(without alignments)  
15559.937 Million cell updates/sec

Title: US-10-781-979-2

Perfect score: 2082

Sequence: 1 gtgaaagatgagtcacata.....acgatctgttaccacataa 2082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|----|-------------------|
| 1          | 168.6 | 8.1         | 3468   | 3  | US-09-001-982-9   |
| 2          | 168.6 | 8.1         | 3468   | 3  | US-09-668-650-9   |
| 3          | 168.6 | 8.1         | 3471   | 3  | US-09-002-285-71  |
| 4          | 168.6 | 8.1         | 3471   | 3  | US-09-589-477-71  |
| 5          | 168.6 | 8.1         | 3471   | 3  | US-10-099-285A-71 |
| 6          | 168.6 | 8.1         | 3726   | 3  | US-09-001-982-11  |
| 7          | 168.6 | 8.1         | 3726   | 3  | US-09-668-650-11  |
| 8          | 160.6 | 7.7         | 2407   | 3  | US-09-661-322A-29 |
| 9          | 95.6  | 4.6         | 4173   | 3  | US-09-661-322A-37 |
| 10         | 94.4  | 4.5         | 1959   | 3  | US-09-661-322A-5  |
| 11         | 93.4  | 4.5         | 3684   | 2  | US-08-448-170-7   |
| 12         | 93.4  | 4.5         | 3684   | 3  | US-08-961-803-5   |
| 13         | 93.4  | 4.5         | 3684   | 3  | US-09-661-322A-62 |
| 14         | 93    | 4.5         | 1561   | 2  | US-08-532-547-2   |
| 15         | 93    | 4.5         | 1561   | 2  | US-08-379-658B-2  |
| 16         | 93    | 4.5         | 1561   | 3  | US-08-455-838-2   |
| 17         | 93    | 4.5         | 1561   | 3  | US-09-019-809-2   |
| 18         | 93    | 4.5         | 1561   | 3  | US-09-471-177-2   |
| 19         | 93    | 4.5         | 1561   | 3  | US-09-220-806-2   |
| 20         | 93    | 4.5         | 1897   | 3  | US-09-363-970-5   |
| 21         | 93    | 4.5         | 3471   | 3  | US-09-002-285-73  |
| 22         | 93    | 4.5         | 3471   | 3  | US-09-589-477-73  |
| 23         | 93    | 4.5         | 3471   | 3  | US-09-661-322A-27 |
| 24         | 93    | 4.5         | 3471   | 3  | US-10-099-285A-73 |

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|----|------|-----|------|---|------------------|-------------------|
| 25 | 93   | 4.5 | 4344 | 2 | US-08-532-547-4  | Sequence 4, Appli |
| 26 | 93   | 4.5 | 4344 | 2 | US-08-379-658B-4 | Sequence 4, Appli |
| 27 | 93   | 4.5 | 4344 | 3 | US-08-455-838-4  | Sequence 4, Appli |
| 28 | 93   | 4.5 | 4344 | 3 | US-09-019-809-4  | Sequence 4, Appli |
| 29 | 93   | 4.5 | 4344 | 3 | US-09-471-177-4  | Sequence 4, Appli |
| 30 | 93   | 4.5 | 4344 | 3 | US-09-220-806-4  | Sequence 4, Appli |
| 31 | 92.8 | 4.5 | 3934 | 2 | US-08-100-709-3  | Sequence 3, Appli |
| 32 | 92.8 | 4.5 | 3934 | 2 | US-08-176-865-3  | Sequence 3, Appli |
| 33 | 92.8 | 4.5 | 3934 | 2 | US-08-474-038-3  | Sequence 3, Appli |
| 34 | 92.8 | 4.5 | 3934 | 2 | US-08-779-046-3  | Sequence 3, Appli |
| 35 | 92.8 | 4.5 | 3934 | 2 | US-08-881-340-3  | Sequence 3, Appli |
| 36 | 90.2 | 4.3 | 3797 | 2 | US-07-915-203-1  | Sequence 1, Appli |
| 37 | 90.2 | 4.3 | 3797 | 2 | US-08-272-887-1  | Sequence 1, Appli |
| 38 | 90.2 | 4.3 | 3797 | 2 | US-08-789-449-1  | Sequence 1, Appli |
| 39 | 88.2 | 4.2 | 4074 | 2 | US-08-377-690-1  | Sequence 1, Appli |
| 40 | 86.2 | 4.1 | 3507 | 2 | US-08-315-468-3  | Sequence 1, Appli |
| 41 | 81.8 | 3.9 | 3504 | 3 | US-10-089-678-2  | Sequence 2, Appli |
| 42 | 81.8 | 3.9 | 3690 | 3 | US-10-089-678-3  | Sequence 3, Appli |
| 43 | 79.6 | 3.8 | 1607 | 3 | US-08-286-870A-5 | Sequence 5, Appli |
| 44 | 79.6 | 3.8 | 1946 | 3 | US-08-286-870A-3 | Sequence 3, Appli |
| 45 | 79.6 | 3.8 | 2965 | 2 | US-08-460-570-1  | Sequence 1, Appli |

ALIGNMENTS

RESULT 1  
US-09-001-982-9  
; Sequence 9, Application US/09001982  
; Patent No. 6204246  
; GENERAL INFORMATION:  
; APPLICANT: Bosch, Hendrick J.  
; APPLICANT: Stiekema, Willem J.  
; TITLE OF INVENTION: Hybrid Toxin  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6204246artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/001,982  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/602,737  
; FILING DATE: 21-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3468 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..3468

US-09-001-982-9

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Query Match      8.1%; Score 168.6; DB 3; Length 3468;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

QY 156 AATTTGGGAATCGTGCAGAACGATAACAAGTAGTTGGGATAAATCTTATAGAGTTTGTGAT 215
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Db 153 AATAGGCGATGCGACAAAGAGCAGTATCTATTGGGACACCATAGTCTCTCTTATCAC 212

QY 216 AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 AGCACCTTCTTACTTGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272

QY 270 TCCGACTAATCGTCAAACTGTGTCAGCACCTTTCTATATGTGATTTTATATCTATATTCG 329
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Db 273 AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATATCTATATTGCA 332

QY 330 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTATGATCGAATTTTGACGGTAAATTTGAA 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGGATTGCAGATTTTAAATGGTTCTGTACT 392

QY 390 AAATATATAGAGTAGTATTATCTTCTTATCTCTGGGCTTGGCTTAAAGACGGTAAACCACT 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 CTTATACAGAACTATTAGAGGCTCTGGATAGCTGGAATAGAAATCCTAATTTCTGCTTC 452

QY 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATTTAGTTTATTTTAAACTTTTCAGAAAG 509
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 TGTCTGAAGAACTCCGTACTCGTTTTAGAAATCGCGACTCAGAAATTTGATAGAATTTTAAC 512

QY 510 AGATTTCAATGAATTTCTAGGAGGTCATTTGCAAGAAACAATGCTCAAGTATGTTATT 569
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CCGAGGCTCTTTAACGAATGGTGGCTCGTTAGCTAGACAAATGGCCAAATATTATTATT 572

QY 570 ACTTCTTTTGCACAGCTGCAAACTGTCAGTTTATTACTATTAAAGGATGCGATTTCAATA 629
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 ACTTCTTTTGCAGCGCTGCAATTTTCCATTTATTACTACTAAGGGATGCTACTAGATA 632

QY 630 TAAAGCACAATGGTTCCTCAATTTTGTAGTGCAGAGAAATGAAGATCGGAAATTAATATCACC 689
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 TGGCACTAATTTGGGGCTATACAACTGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692

QY 690 TTAACAGTGGTTGTATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGA 749
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 693 AGAGCTTATT-----GAACT 707

QY 750 GTATACCAATTTATTTTATATTGTTATCAGGTAGGTTTAAATCAGATAAAACAGGGGG 809
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 ATATACTGATTTATGCGTACATTTGGTATATCGAGGTTTCAACGAACTAAGACAACGAGG 767

QY 810 GACAGTGTGACACTTTGGTTCGAAATTTAATAAATTCGTAGAGAAATGACGTTGGCGGT 869
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 768 CACTAGTGTACAGCTTGGTTAGAAATTTTCATAGATATCGTAGAGATGACATTTGATGCT 827

QY 870 ATTGATATATCGCTATATTTCCAACTTATGATTTTGTAGAAATATCCATTTGCCACACA 929
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 ATTAGATATAGTAGCATCAATTTTCAAGTCTTGATATTACTAATTTACCCCAATAGAAACAGA 887

QY 930 TGTAGAGTTGACTTAGGAAATTTATACAGATGCGATGGGATATTTCATCGGGAATTTATAG 989
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 888 TTTTCAGTTGAGTAGGGTCATTTATACAGATCCAAATGGTTTGTACATCGTAGTAGTCT 947

QY 990 TTGGTTACGGAATTTGGCCTAAATCTTTTAAATGG 1022
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 948 TAGGGGAGAAAGTTGGTTAGCTTTTGTAAATAG 980
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RESULT 2  
US-09-668-650-9  
; Sequence 9, Application US/09668650  
; Patent No. 6780408  
; GENERAL INFORMATION:  
; APPLICANT: Bosch, Hendrick J.

```
Stiekema, Willem J.  
TITLE OF INVENTION: Hybrid Toxin  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 678040artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/668,650  
FILING DATE: 22-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/001,982  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/602,737  
FILING DATE: 21-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3468 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Bacillus thuringiensis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3468  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-668-650-9
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Query Match      8.1%; Score 168.6; DB 3; Length 3468;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;

QY 156 AATTTGGGAATCAGTCGAAACGATAACAAGTAGTTGGGATAAATCTTATAGAGTTTGTGAT 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 AATAGGCGATGCGACAAAGAGCAGTATCTATTGGGACACCATAGTCTCTCTTATCAC 212

QY 216 AGAACCTAGTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 AGCACCTTCTTACTTGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272

QY 270 TCCGACTAATCGTCAAACTGTGTCAGCACCTTTCTATATGTGATTTTATATCTATATTCG 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATATCTATATTGCA 332

QY 330 TAAAGAGGTAGCGGATAGTGTGTTTAAAGTATGATCGAATTTTGACGGTAAATTTGAA 389
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGGATTGCAGATTTTAAATGGTTCTGTACT 392

QY 390 AAATATATAGAGTAGTATTATCTTCTTATCTTGGGCTTGGCTTAAAGACGGTAAACCACT 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 CTTATACAGGAATCTTATAGAGGCTCTGGATAGCTGGAATAGAAATCCTAATTTCTGCTTC 452

QY 450 TCAAAAGACAAATAATTTCTGATATCGGACAAATTTAGTTTATTTTAAACTTTTCAGAAAG 509
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Db 453 TGTCTGAAGAACTCCCGTACTCGTTTTAGAAATCGCGACTCAGAAATTTGATAGAATTTTAAC 512
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QY 510 AGATTTCAATGAAATCTAGAGGGTCATTGTCAAGAAACAAATGCTCAAGTATTGTTATT 569  
Db 513 CCGAGGGCTTTAAACGAATGGTGGCTCGTTAGTAGACAAATGCGCAAAATATTATTATT 572  
QY 570 ACTTACTTTTGCAACAGCTGCAAAATGCGAGTTATTACTATTAAAGGGATGCGAGTTCAATA 629  
Db 573 ACCTTCTTTTGGAGCGCTGCAATTTTCCATTTATTACTACTAAAGGGATGCTACTAGATA 632  
QY 630 TAAAGCACATGCTTCCCATTTTGTAGTCAGAGAAATGTAAGATCGGAATTAATATCACC 689  
Db 633 TGGCACTAAATGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692  
QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAAAATGCAAAACGCGAGA 749  
Db 693 AGAGCTTATT-----GAACT 707  
QY 750 GTATACCAATATTGTTTATATTGTTATAGTATAGTATTAAATTCAGATAAAACAGGGGG 809  
Db 708 ATATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 887  
QY 930 TGTAGAGTTGACTAGGAAATTTATACAGATCGAGTGGGATATTCATCGGGAATTTATAG 989  
Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATTTGTTTGTACATCGTAGTGTCT 947  
QY 990 TTGTTACGGATTTGCGCTTAATCTTTTAAATG 1022  
Db 948 TAGGGAGAAAGTTGGTTTGGCTTTGTTAAATAG 980

## RESULT 3

US-09-002-285-71  
; Sequence 71, Application US/09002285  
; Patent No. 6369213  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; APPLICANT: Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/002,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996

; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-002-285-71

Query Match 8.1%; Score 168.6; DB 3; Length 3471;  
Best Local Similarity 52.5%; Pred. No. 1.9e-30;  
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;  
QY 156 AATTTGGGAATCAGTCGAAACGATACACAGTATTCGGATAAATCTTATAGAGTTTCTGAT 215  
Db 153 AATAGCGGATGCGCAAAAGAGCAGTATCTATTGGGCAACCATAGTCTCTCTTATCAC 212  
QY 216 AGAACCTAGTTTGGGTGGAATTAATACACTATTAT-----CAATAATAGGAAACCTAAT 269  
Db 213 AGCACTTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAAGTACTAGG 272  
QY 270 TCCGACTAATCGTCAAACTGTCTCAGCACTTTCTATATGTGATTTTATATCTATATAATCG 339  
Db 273 AGGTAGTAGTGACAATCCATATCAGATTTGTCTATATGTGACTTATTATCTATTATTGA 332  
QY 330 TAAAGAGGTAGCGGATAGTGTTTTAAAGTATCGGATTCGAGATTTTGACGGTAAATGAA 389  
Db 333 TTTACGGGTAGTCAGAGTGTTTTAAATGATGGGATTCAGATTTTAAATGTTCTGTACT 392  
QY 390 AAATATATAGAGAGTATTATCTTTCTTATCTTGGGGCTTGGCTTAAAGACGGTAAACCACT 449  
Db 393 CTTATACAGGAATCTTTTAGAGGCTCTGGATAGCTGGATAAGATCCCTAATTCGTCTTC 452  
QY 450 TCAAAAGACAAATAATTCGTATATCGGACAATTAGTTTATTTATTTTAACTTTTCAGAAAG 509  
Db 453 TGTGAAAGAACTCCGTACTCGTTTGAATCGCGACTCAGAATTTGATAGAATTTTAAAC 512  
QY 510 AGATTTCAATGAATTTCTAGGAGGCTCATTTGCAAGAAACAATGCTCAAGTATTGTTATT 569  
Db 513 CCGAGGGTCTTTAAACGAATGGTGGCTCGTTAGCTAGACAAATGCCCCAATATTATTATT 572  
QY 570 ACTTACTTTTGCACAAGCTGCAAAATGTGCAGTTATTACTATTAAAGGGATGCGAGTTCAATA 629  
Db 573 ACCTTCTTTTGGAGGGCTGCAATTTTCCATTTTATTTACTACTAGGGAATGCTACTAGATA 632  
QY 630 TAAAGCAACAATGGTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689  
Db 633 TGGCACTAAATGGGGCTATACAAATGCTACACCTTTTATAAATTTATCAATCAAACTAGT 692  
QY 690 TAAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGCGAGA 749  
Db 693 AGAGCTTATT-----GAACT 707  
QY 750 GTATACCAATATTGTTTATATTGTTATCGAGTATCGAGTATTAAATTCAGATAAAACAGGGGG 809  
Db 708 ATATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 767  
QY 810 GACAGGTGCTGACACTTGGTCGAAATTTTAAATAAATTTTTCGAGAGAAATACGCTTGGCGGT 869  
Db 768 CACTAGTGTCTACAGCTTGGTGAATTTTCATAGATATCGTAGAGATGACATTTGATGTT 827  
QY 870 ATTGATATATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTCGCAACACA 929  
Db 828 ATTAGATATAGTAGCATCATTTTTCAGTCTTGATATTACTAATACCAATAGAAACAGA 887  
QY 930 TGTAGAGTTGACTAGGAAATTTATACAGATCGAGTGGGATATTCATCGGGAATTTATAG 989  
Db 888 TTTTCAGTTGAGTAGGGTCAATTTATACAGATCCAAATTTGTTTGTACATCGTAGTGTCT 947  
QY 990 TTGTTACGGATTTGCGCTTAATCTTTTAAATG 1022  
Db 948 TAGGGAGAAAGTTGGTTTGGCTTTGTTAAATAG 980

Db 888 TTTTCAGTTGAGTAGGTCATTATATACAGATCCAAATGGTTTGTATACATCGTAGTAGTCT 947  
Qy 990 TTGGTTACGGAATTGGCCCTAACTATTTTAATGG 1022  
Db 948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

## RESULT 4

US-09-589-477-71  
; Sequence 71, Application US/09589477  
; Patent No. 6570005  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Wicker, Carol  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Walz, Michelle  
; APPLICANT: Stockhoff, Brian  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/589,477  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/886,615  
; FILING DATE: 1-JUL-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/674,002  
; FILING DATE: 1-JUL-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: MA-701C1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3471 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-589-477-71

Query Match 8.1%; Score 168.6; DB 3; Length 3471;  
Best Local Similarity 52.5%; Pred. No. 1.9e-30;  
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;  
Qy 156 AATTGGGAATCAGTCGAACGATACAAAGTATGGGATAAATCTTATAGAGTTTGTGAT 215  
Db 153 ATAGCGGATGAGCAAAAGACGATATCTATGGGACAAACCATAGTCTCTTATAC 212  
Qy 216 AGAACCTAGTTGGGTGGAAATTAATACATTTAT-----CAATAATAGGAAACTAAT 269  
Db 213 AGCACCTTCTCTTACTGGATTAATTTCAATAGTATATGACCTTATAGGTAAGTACTAGG 272  
Qy 270 TCCGACTAATCGTCRAACGTGTGCAGCACTTCTCTATATGTGATTATATCTATAATTCG 329

Db 273 AGGTAGTAGTGGACAATCCATATCAGATTTGTCTATATGTGACTTATATCTATATTGA 332  
Qy 330 TAAAGAGGTAGCCGATAGTGTGTTTAAAGTGATGCGATTGCGAGATTTGACGGTAAATGAA 389  
Db 333 TTTACGGGTAGTCAGAGTGTGTTTAAATGATGGGATTCAGATTTTAAATGGTCTGTACT 392  
Qy 390 AAAATTATAGAGAGTATTATCTTTCTTATCTTTGGGGCTTTGGCTTAAAGACGGTAAACCACT 449  
Db 393 CTTATACAGGAACATTTTAGAGGCTCTGGAATAGCTGGAATAAGAATCCTAATCTGCTTC 452  
Qy 450 TCAAAAGACAAATAATCTTGATATCGGCAATTAGTTTATTTTAACTTTTAACTTTTCAAG 509  
Db 453 TGCTGAAGAACCTCGGTACTCGTTTGTAGAACTCGCCGACTCAGAAATTTGATAGAAATTTAA 512  
Qy 510 AGATTTCAATGAAATTTCTAGGAGGCTCATTTGCAAGAAACAATGCTCAAGTATTTGTTAT 569  
Db 513 CCGAGGCTTTTACGAATGTTGGCTCGTTAGCTAGACAAATGCGCAATATTTATTTATTT 572  
Qy 570 ACCTACTTTTGCACAAAGCTGCAAAATGTCAGTTTATTTACTTATTAAGGGATGCAAGTTCA 629  
Db 573 ACCTTCTTTTGGAGCGCTGCAATTTTCCATTTTATTTACTTACTAAGGGATGCTTACTAG 632  
Qy 630 TAAAGCACAAATGTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTAATATCACC 689  
Db 633 TGGCACTAATTTGGGGGCTATACAATGCTACACCTTTTATTAATTTATCAATCAAACTAG 692  
Qy 690 TAAAGTGTGTTGTGATTTTACCGGTGATTTACTATGAGCGATTTAAATGCAAAACGCGAGA 749  
Db 693 AGAGCTTATTT-----GAACT 707  
Qy 750 GTATACCAATTTTGTGTTTATTTGATCAGTATCAGTATGTTTAAATCAGATAAAACAGGGGG 809  
Db 708 ATATACTGATTATTCGTTACATTTGTTATAATCGAGGTTTCAACGAATTAAGACAACGAGG 767  
Qy 810 GACAGTCTGCACACTTGGTGAATTTTAAATAATTTGTCAGAGAAATGACGTTGCGCGT 869  
Db 768 CACTAGTCTACAGCTTGGTTAGAAATTTTATAGATATCGTAGAGAGATGACATGATGGT 827  
Qy 870 ATTGATATTTATCGTATATTTTCCAACTTATGATTTTGAGAAATATCATTTGCCAACACA 929  
Db 828 ATTAGATATAGTATCATTTTTCAGTCTTGATATTTACTAATTAACCAATAGAAACAGA 887  
Qy 930 TGTAGATGACTAGGAAATTTATACAGATGCAAGTGGGATATTCATCGGGAACCTTATAG 989  
Db 888 TTTTCAGTTGAGTAGGGTCAITTTATACAGATCCAAATGGTTTGTGTACATCGTAGTAGTCT 947  
Qy 990 TTGGTTACGGAATTTGGCCTAATACTTTTAAATGG 1022  
Db 948 TAGGGGAGAAAGTTGGTTAGCTTTGTTAATAG 980

## RESULT 5

US-10-099-285A-71  
; Sequence 71, Application US/10099285A  
; Patent No. 6752992  
; GENERAL INFORMATION:  
; APPLICANT: Schnepf, H. Ernest  
; Wicker, Carol  
; Narva, Kenneth E.  
; Walz, Michelle  
; Stockhoff, Brian  
; Muller-Cohn, Judy  
; TITLE OF INVENTION: Toxins Active Against Pests  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:



Query Match 8.1%; Score 168.6; DB 3; Length 3726;  
Best Local Similarity 52.5%; Pred. No. 1.9e-30;

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Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTGGGAATCAGTCGAACGATAACAAGATATTGGGATAAATCTTATAGATTTGTGAT 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 AATAGCGGATGCGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 216 AGAAGCTAGTTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
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Db 213 AGACCTTCTCTTACTGGGAATTAATTTCAATAGTATATGACCTTTATAGGTAAGTACTAGG 272
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QY 270 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGTGATTTTATTTATCTATTAATTCG 329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 AGGTAGTAGGCAATCCATACAGATTGTCTATATGTGACTTATATCTATTATTGA 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 330 TAAAGAGGTAGCCGATAGTGTTTTAAAGTGATGCGATTGCGAGATTTTGA CGGTAATGAA 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGATTGCGAGATTTTAAATGGTCTGTACT 392
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QY 390 AAATTATACAGATATTATCTTCTTATCTTGGGCTTGGCTTAAAGCGGTAACCACT 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 CTTATACAGAACTATTAGAGCTCTGGATAGCTGGAATAAGAATCCTAATTCGTCTTC 452
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QY 450 TCAAAAGACAAATAATCTGTATCGGCAATTAGTTTATTTTAAACTTTTCAGAAAG 509
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Db 453 TGCTGAAGACTCCGTACTCGTTTAGAATCGCGACTCAGAAATTTGATAGAAATTTAAAC 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 510 AGATTTCAATGAATTTCTAGAGGGTCAATGTCAAGAAACAATGCTCAAGTATTTGTAAT 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGCTAGCAAAATGCCAAATATTATTATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 570 ACTTACTTTTGCACAGCTGCAAAATGTCAGTATTACTTATTAAAGGATGCAATCAATA 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 ACCTTCTTTTGGAGCGCTGCATTTTTCATTTATTACTTAAAGGGATGCTACTAGATA 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 630 TAAAGCACAAATGTTTCCCAATTTTGGATGCGAGAAATGAAGATCGGAATTAATATCAC 689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 TGGCACTAATTTGGGGCTATACATGCTACACCTTTTAAATTTATCAATCAAACTAGT 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 690 TAACAGTGTGTGATTTTACCGGTGATTTACTATGAGCGATTAAATGCAAAACGCGACA 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 693 AGAGCTTAT-----GAACT 707
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 750 GTATACCAATATTGTTTATATGCTATCAGGTAGGTTTAAATCAGATAAACAGGGGG 809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 ATATACTGATTAATTCGTACATTTGTTAGTAAATCGAGGTTTCAACGAACTAAGACACGAG 767
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 810 GACAGTGTGACACATTTGTCGAAATTTAAATAAATTCGTAGAGAAATGACGTTGGCGGT 869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 768 CACTAGTGTACAGCTTGGTAGAATTTCTAGATATCGTAGAGATGACATTTGATGTT 827
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 870 ATTGGATATTATCGCTATATTTCCAACTTATGATTTTGGAGAAATATCCATTGCCAACACA 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 ATTAGATATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTTACCCCAATAGAACACA 887
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 930 TGTAGATTGACTAGGGAATTTATACAGATGCGATGGGATATTCTACGGGAACTTATAG 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 888 TTTTCAGTTAGTAGGGTCAITTTATACAGATCCAAATGGTTTGTATACATCGTAGTGTCT 947
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 990 TTGGTTTACGGAATTTGGCCTAAATACTTTTAAATGG 1022
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 948 TAGGGGAGAAAGTTGGTTTAGCTTTGTTAATAG 980
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 7

US-09-668-650-11

; Sequence 11, Application US/09668650

; Patent No. 6780408

; GENERAL INFORMATION:

; APPLICANT: Bosch, Hendrick J.

; TITLE OF INVENTION: Hybrid Toxin

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

```
;
; ADDRESSEE: No. 6780408artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,650
; FILING DATE: 22-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,982
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/602,737
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3726
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
;
; US-09-668-650-11
```

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Query Match      8.1%; Score 168.6; DB 3; Length 3726;
Best Local Similarity 52.5%; Pred. No. 1.9e-30;
Matches 458; Conservative 0; Mismatches 364; Indels 51; Gaps 2;
QY 156 AATTGGGAATCAGTCGAACGATAACAAGATATTGGGATAAATCTTATAGATTTGTGAT 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 153 AATAGCGGATGCGCAAAAGACGATATCTATTGGGCAACCATAGTCTCTCTTATCAC 212
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 216 AGAAGCTAGTTTGGGTGGAAATTAATACACTATTAT-----CAATAATAGGAAACTAAT 269
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 AGACCTTCTCTTACTGGGAATTAATTTCAATAGTATATGACCTTTATAGGTAAGTACTAGG 272
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 270 TCCGACTAATCGTCAAACTGTGTGACGACTTTCTATATGTGATTTTATTTATCTATTAATTCG 329
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 273 AGGTAGTAGGCAATCCATACAGATTGTCTATATGTGACTTATATCTATTATTGA 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 330 TAAAGAGGTAGCCGATAGTGTTTTAAAGTGATGCGATTGCGAGATTTTGA CGGTAATGAA 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 TTTACGGGTAAAGTCAGAGTGTTTTAAATGATGGATTGCGAGATTTTAAATGGTCTGTACT 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 AAATTATACAGATATTATCTTCTTATCTTGGGCTTGGCTTAAAGCGGTAACCACT 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 CTTATACAGAACTATTTAGAGGCTCTGGATAGCTGGAATTAAGAATCCTAATTCGTCTTC 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 450 TCAAAAGACAAATAATCTGTATCGGCAATTAGTTTATTTTAAACTTTTCAGAAAG 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 TGCTGAAGAACTCCGTACTCGTTTAGAATCGCGCACTCAGAAATTTGATAGAAATTTAAAC 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 510 AGATTTCAATGAATTTCTAGAGGGTCAATGTCAAGAAACAATGCTCAAGTATTTGTAAT 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CCGAGGCTCTTTAAACGAATGGTGGCTCGTTAGCTAGCAAAATGCCAAATATTATTATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 570 ACCTACTTTTGCACAGCTGCAAAATGTCAGTATTACTTATTAAAGGATGCAATCAATA 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 573 ACCTCTCTTGGCAGCGTGCATTTTCCATTTTACTACTAAGGATGCTACTAGATA 632  
Qy 630 TAAAGCACATGTTCCCATTTTGGAGTCAGAGATGTAAGATCGGAATTAATATCACC 689  
Db 633 TGGCATAAATTTGGGGCTATACAATGCTACACCTTTTATAAATTTATCAAACTAGT 692  
Qy 690 TAACAGTGGTGTGATTTTACCGGTGATTACTATGAGCGATTAAATGCAAAACGGCAGA 749  
Db 693 AGAGCTTATT-----GAACT 707  
Qy 750 GTATACCAATATTGTTTATATTGGTATCAGGTAGGTTTAAATTCAGATAAACAGGGGG 809  
Db 708 ATATACCTGATTATTGGGTACATTTGTTAGTCTTGTATATTACTTACCAATAGAAACAGA 887  
Qy 930 TGTAGATTGCTAGGGAATTTATACAGATGCGGTGGATATTCATCGGGAATTTATAG 989  
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAAATTTGTTTGTATCATCGTAGTAGTCT 947  
Qy 990 TTGGTTACGGAATTTGGCTTAATCTTTTAATGG 1022  
Db 948 TAGGGAGAAAGTTGGTTTGGTTTAAATAG 980

## RESULT 8

US-09-661-322A-29  
; Sequence 29, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-09-661-322A-29

Query Match 7.7%; Score 160.6; DB 3; Length 2407;  
Best Local Similarity 51.9%; Pred. No. 1.4e-28;  
Matches 453; Conservative 0; Mismatches 369; Indels 51; Gaps 2;  
Qy 156 AATTTGGGAATCAGTCGAACCGATAAAGATTTGGGATAAATCTTTATAGAGTTTGTGAT 215  
Db 153 AATAGCGATGCAAGCAAGAGACAGTATCTATTGGGACACCATAGTCTCTTTATCAC 212  
Qy 216 AGAACCTAGTTGGGTGGGAATTAATACATTTAT-----CAATATAGGAAACATAAT 269  
Db 213 AGCACCTCTCTTACTGGATTAAATTTCAATAGTATATGACCTTATAGGTAAGTAGTAGG 272  
Qy 270 TCCGACTAATCGCAACATGTCGACGACTTTCTATATGATTTATTTATCTATTAATTCG 329  
Db 273 AGGTAGTAGGGAATCCATATCAGATTTGCTATGTGACTTATATCTATTTATTTGA 332  
Qy 330 TAAAGAGGTAGCCGATAGTGTGTTTAAAGTGTGCGATTGCGAGATTTTGACGGTAAATTTGAA 389

Db 333 TTTACGGTAACTCAGAGTGTTTTAAATGATGGATTGCGAGATTTTAAATGTTCTGTACT 392  
Qy 390 AAATTTATAGAGATTAATCTTTCTTATCTTCGGGGCTTGGCTTAAAGACGGTAACCACT 449  
Db 393 CTTATACAGGAATACTTTTAGAGGCTCTGGATAGCTGGAATAAGAATCCCTAAATTTCTGCTTC 452  
Qy 450 TCAAAAGACAAAATAATCTCTGATATCGGACAAATTAGTTTATTTATTTTAAAACTTTTCAGAAAG 509  
Db 453 TGCTGAGAACTCCGCTACTCGTTTGTAGATCCCGACTCAGAAATTTGTAGATTTTAAAC 512  
Qy 510 AGATTTCAATGAAATTTCTAGGAGGTCATTTGTCAAGAAACAATGCTCAAGATTTGTATT 569  
Db 513 CCGAGGCTCTTTAAGCAATGTTGGCTCGTTAGCTAGACAAAATGCCCAATATTAATTT 572  
Qy 570 ACTTACTTTTGCACAAGCTGCAAAATGTCAGTTATTTACTTATTAAGGATGCAAGTTCAATA 629  
Db 573 ACCTCTCTTTTGGAGCGCTGCATTTTCCATTTATTTACTACTAAGGGATGCTACTAGATA 632  
Qy 630 TAAAGCACAAATGTTTCCCATTTTTCAGTGCAGAGAAATGTAAGATCGGAATTTAATATCACC 689  
Db 633 TGGCACTAATTTGGGGCTATACAATGCTACACCTTTTATTAATTTATCAATCAAACTAGT 692  
Qy 690 TAAAGTGGTGTGATTTTACCGGTGATTTACTATGAGCGATTAAATGCAAAACGGCAGA 749  
Db 693 AGAGCTTATT-----GAACT 707  
Qy 750 GTATACCAATATTGTTTATATTGGTATCAGGTAGGTTTAAATTCAGATAAACAGGGGG 809  
Db 708 ATATACCTGATTATTGGGTACATTTGGGATAATTCAGAGTTTCAACCGAACTAAGACACGAGG 767  
Qy 810 GACAGTGTCTGACACTTTGGTCGAAATTTAAATAAATTTTCGTAGAGAAATCAGCTTGGCGGT 869  
Db 768 GCCTAGTGTACAGCTTTGGTTAGAAATTTTCATAGATATCGAGAGAGATGACATTTGATGG 827  
Qy 870 ATTGATATTTATCGCTATATTTCCAACTTATGATTTTGAGAAATATCCATTTGCCAACACA 929  
Db 828 ATTAGAAATAGTAGCATCATTTTCAAGTCTTGATATTACTAATTTACCAATAGAAACAGA 887  
Qy 930 TGTAGATTGCTAGGGAATTTATACAGATCAGTGGGATTTATTCATCGGGAATTTATAG 989  
Db 888 TTTTCAGTTGAGTAGGTCATTTATACAGATCCAAATTTGTTTGTATCATCGTAGTAGTCT 947  
Qy 990 TTGGTTACGGAATTTGGCTTAATCTTTTAATGG 1022  
Db 948 TAGGGAGAAAGTTGGTTTGGTTTAAATAG 980

## RESULT 9

US-09-661-322A-37  
; Sequence 37, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 4173  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3687)  
US-09-661-322A-37

Query Match 4.6%; Score 95.6; DB 3; Length 4173;  
Best Local Similarity 62.7%; Pred. No. 4.6e-13;  
Matches 168; Conservative 0; Mismatches 94; Indels 6; Gaps 1;  
QY 717 TTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGTA 776  
DB 645 TTATATGAGCGCCAGTGGAAACAGAGAGATTATTCGACTATTGCGTAGAATGGTA 704  
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 836  
DB 705 TAATACAGGTCTAAATAGCTTGAGA-----GGGACAAATGCGCAAGTTGGTGGTTA 758  
QY 837 TTAATAATTCGTAGAGAAATGACGTTGGGGTATTGGATATATTCGCTATATTTCCAAAC 896  
DB 759 TAATCAATTCGCTAGAGACTTAACGTTAGGGGTATTAGATCTAGTGGCACTATTCCCAAG 818  
QY 897 TTATGATTTTGAGAAATATCCATTGCGCAACACATGTAGAGTTGACCTAGGGAATTTATAC 956  
DB 819 CTATGACACTCGCACTTATCCATAAATACGAGTGTCTAGTTAAACAGGGAAGTTTATAC 878  
QY 957 AGATCGAGTGGGATATTCATCGGGAAT 984  
DB 879 AGACGCAATTGGAGCAACAGGGGTAAAT 906

RESULT 10  
US-09-661-322A-5  
; Sequence 5, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 5  
; LENGTH: 1959  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-09-661-322A-5

Query Match 4.5%; Score 94.4; DB 3; Length 1959;  
Best Local Similarity 62.2%; Pred. No. 7.5e-13;  
Matches 168; Conservative 0; Mismatches 96; Indels 6; Gaps 1;  
QY 716 ATTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGT 775  
DB 629 ATATATACAGAGAACAAATCAGATATACAGAGAAATTTCTAACCTTCGCTACATGT 688  
QY 776 ATCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 835  
DB 689 ATAATACAGGGCTAAATAACTTAA-----GAGGGACAAATGCTGAAGTTGGTTGCGGT 742  
QY 836 TTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGATATATTCGCTATATTTCCAA 895  
DB 743 ATAATCAATTCGCTAGAGACCTTAACGTTAGGGGTATTAGATTAGTAGCCCTATTCCCAA 802  
QY 896 CTTATGATTTGAGAAATATCCATTGCGCAACACATGTAGAGTTGACTAGGGAATTTATA 955  
DB 803 GCTATGATCTCGCACTTATCCATCAATACGAGTGTCTAGTTAAACAGAGAAATTTATA 862  
QY 956 CAGATCGAGTGGGATATTCATCGGGAATTT 985  
DB 863 CAGATCCAATTCGGAGAACAAATGCACCTT 892

RESULT 11  
US-08-448-170-7  
; Sequence 7, Application US/08448170  
; Patent No. 5723758  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 5723758el Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.C. PS158C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,170  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/759,247  
; FILING DATE: 13-SEPT-1991  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: M/S 102D.C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3684 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-448-170-7

Query Match 4.5%; Score 93.4; DB 2; Length 3684;  
Best Local Similarity 62.1%; Pred. No. 1.5e-12;  
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;  
QY 717 TTACTATGAGCGATTAAATGCAAAACGGCAGAGTATACCAATTATTGTTTATATTGGTA 776  
DB 645 TTATATGAGCGCCAGTGGAAACAGAGAAATATTTCTGATTTATTCGCAAGATGGTA 704  
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTTGGTCGAAAT 836  
DB 705 TAATACGCGTTTAAATAATTTGAGA-----GGGACAAATGCTGAAGTTGGTTGCGATA 758  
QY 837 TTAATAAATTCGTAGAGAAATGACGTTGGCGGTATTGGATATATTCGCTATATTTCCAAAC 896  
DB 759 TAATCAATTCGCTAGAGACTTAACGCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAG 818  
QY 897 TTATGATTTTGAGAAATATCCATTGCGCAACACATGTAGAGTTGACTAGGGAATTTATAC 956  
DB 819 CTATGACAGCGGTGTTTATCCANTGAATACAGTGTCTCAATTAACAGAGAAATTTATAC 878

QY 957 AGATGCGATGGGATATTCATCGGGAACCTT 985  
|||||  
Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907  
|||||

## RESULT 12

US-08-961-803-5  
; Sequence 5, Application US/089961803  
; Patent No. 6150589  
; GENERAL INFORMATION:  
; APPLICANT: Payne, Jewel  
; APPLICANT: Cummings, David A.  
; APPLICANT: Cannon, Raymond J.C.  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stelman, Steve  
; TITLE OF INVENTION: No. 615058961 Bacillus thuringiensis Isolate Denoted  
; TITLE OF INVENTION: B.t. PS158C2, Active Against Lepidopteran Pests, and Genes  
; TITLE OF INVENTION: Encoding Lepidopteran-Active Toxins  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jay M. Sanders  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,803  
; FILING DATE: 31-OCT-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,902  
; FILING DATE: 01-JUNE-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/759,247  
; FILING DATE: 13-SEPT-1991  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/448,170  
; FILING DATE: 23-MAY-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sanders, Jay M.  
; REGISTRATION NUMBER: 39,355  
; REFERENCE/DOCKET NUMBER: N/S 102DCD1  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3684 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-961-803-5

Query Match 4.5%; Score 93.4; DB 3; Length 3684;  
Best Local Similarity 62.1%; Pred. No. 1.5e-12;  
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 717 TTACTATGCGGATTAATAATGCAAAACGCGCAGAGTATACCAATTATTGTTATTGGTA 776  
|||||  
Db 645 TTATTATGCGCCAGTGGAAAAACGAGAGATATCTGATTATTGCGCAAGATGGTA 704  
|||||  
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATT 836  
|||||

Db 705 TAATACGGGTTTAAATAATTGAGA-----GGACAATGCTGAAAGTTGGTGGGATA 758  
|||||  
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGGGTATTGGATATATCGCTATATTTTCCAAC 896  
|||||  
Db 759 TAATCAATTTCCGTAGAGACTTAAACGCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAG 818  
|||||  
QY 897 TTATGATTTTGGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGCAAAATTTATAC 956  
|||||  
Db 819 CTATGACACGGTGTATTCCATGAATACCAATGCTCAATTAAACAAGAAATTTATAC 878  
|||||  
QY 957 AGATGCGATGGGATATTCATCGGGAACCTT 985  
|||||  
Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907  
|||||

## RESULT 13

US-09-661-322A-62  
; Sequence 62, Application US/09661322A  
; Patent No. 6593293  
; GENERAL INFORMATION:  
; APPLICANT: Baum, James A.  
; APPLICANT: Chu, Chih-Rei  
; APPLICANT: Donovan, William P.  
; APPLICANT: Gilmer, Amy J.  
; APPLICANT: Rupar, Mark J.  
; TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compo  
; TITLE OF INVENTION: and Methods of Use  
; FILE REFERENCE: MECO201  
; CURRENT APPLICATION NUMBER: US/09/661,322A  
; CURRENT FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 62  
; LENGTH: 3684  
; TYPE: DNA  
; ORGANISM: Bacillus thuringiensis  
US-09-661-322A-62

Query Match 4.5%; Score 93.4; DB 3; Length 3684;  
Best Local Similarity 62.1%; Pred. No. 1.5e-12;  
Matches 167; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 717 TTACTATGCGGATTAATAATGCAAAACGCGCAGAGTATACCAATTATTGTTATTGGTA 776  
|||||  
Db 645 TTATTATGCGCCAGTGGAAAAACGAGAGATATCTGATTATTGCGCAAGATGGTA 704  
|||||  
QY 777 TCAGGTAGGTTTAAATCAGATAAAACAGGGGGGACAGGTGCTGACACTTGGTCGAAATT 836  
|||||  
Db 705 TAATACGGGTTTAAATAATTGAGA-----GGACAATGCTGAAAGTTGGTGGGATA 758  
|||||  
QY 837 TAATAAATTTCTAGAGAAATGACGTTGGGGTATTGGATATATCGCTATATTTTCCAAC 896  
|||||  
Db 759 TAATCAATTTCCGTAGAGACTTAAACGCTAGGAGTATTAGATCTAGTGGCACTATTCCCAAG 818  
|||||  
QY 897 TTATGATTTTGGAGAAATATCCATTGCCAACACATGTAGAGTTGACTAGGCAAAATTTATAC 956  
|||||  
Db 819 CTATGACACGGTGTATTCCATGAATACCAATGCTCAATTAAACAAGAAATTTATAC 878  
|||||  
QY 957 AGATGCGATGGGATATTCATCGGGAACCTT 985  
|||||  
Db 879 AGATCCCAATGGGAGAACAAATGCACCTT 907  
|||||

## RESULT 14

US-08-532-547-2  
; Sequence 2, Application US/08532547  
; Patent No. 5861543  
; GENERAL INFORMATION:  
; APPLICANT: LAMBERT, BART  
; APPLICANT: JANSSENS, STEFAN  
; APPLICANT: VAN AUDENHOVE, KATRIEN  
; APPLICANT: PEPEROEN, MARNIX







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